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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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          No.
                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       Score
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Match
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Copyright (c) 1993 - 2000 Comp
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Description
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1061 1061 195.5 155 155 144 126.5 123.5 123.5

100.0 100.0 18.4 14.6 14.6 13.6 11.9 11.9 11.9 11.5

205 205 212 212 153 153 130 223 195 229 206

Y99597 Y79298 B01787 R87527 W73358 B40407 B01786 B01786 B01788 B11637

E. coli L-homoseri
E. coli RhtB prote
Escherichia coli Y
Mel-linked mlgA ge
S. colwelliana Mlg
Human ORFX ORF717
Escherichia coli Y

WPI; 2000-414602/36. N-PSDB; A48442.

Livshits VA,

Zakataeva NP,

Aleshin VV,

Belareva

Ă۷,

Tokhmakova

IL;

(AJIN ) AJINOMOTO KK.

23-DEC-1998; 20-DEC-1999;

98RU-0123511 99EP-0125406

Escherichia

coli L-threonin cherichia coli Y

Novel Escherichia bacterium having enhanced L-threonine resistance to enhanced RhtC protein activity, used to produce L-threonine,

due

L-homoserine, L-valine and L-leucine

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В
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Y79298
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Best Local S
Matches 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the L-homoserine resistance protein, RhtB, from Escherichia coli. The coding sequence may be used to impart L-homoserine resistance on E. coli bacteria, which would be useful for producing a high yield of L-homoserine. L-homoserine resistance means that the bacteria will be able to grow on a minimal medium containing L-homoserine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-homoserine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-threonine, L-valine and L-leucine at increased levels.
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                                                                                                                                                                                                                                                                                                                                                18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                         Y79298;
                      Novel RhtB protein, useful for generation of L-homoserine resistance Escherichia bacteria and large-scale production of e.g. L-homoserine
                                                          WPI; 2000-273530/24.
N-PSDB; Z94405.
                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                  L-isoleucine; L-valine;
                                                                                                                                                                                                                                                                                               Homoserine resistance; RhtB protein; L-homoserine; L-alanine;
                                                                                                                                                                                                                                                                                                                                                                                               Y79298 standard; Protein; 205 AA.
           and L-alanine
                                                                                              Livshits VA,
Tokhmakova IL;
                                                                                                                                 (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                          13-OCT-1998;
                                                                                                                                                                                    20-SEP-1999;
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                                                                                                                                                                                                                                                             coli.
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                     protein imparting homoserine resistance
                                                                                                           Zakataeva NP,
                                                                                                                                                          98RU-0118425
                                                                                                                                                                                    99EP-0118581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1061; DB 21; 100.0%; Pred. No. 3.9e-113; tive 0; Mismatches 0;
                                                                                                           Aleoshin VV,
                                                                                                           Belareova
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         improvement of the amino acid productivity of E. coli. The including a deletion, substitution, insertion and/or addition of 1 cor more amino acids and having the activity of making a bacterium or resistant to L-homoserine; DNA encoding RhtB; a bacterium resistance is enhanced by amplifying the copy number or increasing the expression rate of the rhtB DNA, the DNA being carried on a multicopy vector or on a transposon; and a method for producing an acid by cultivating the bacterium in a culture medium to produce and accumulate the amino acid in the medium, from which it is recovered. The method is used for the production of a laincal to L-homoserine, L-alanine, L-isoleucine, L-valine or L-threonine (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt E.} coli; yeaS gene; amino acid production; excretion protein gene; amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B01787 standard; Protein;
                                                                                                                                                    30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli YeaS amino acid excretion protein
                           Tokhmakova IL;
                                                      Livshits VA,
                                                                                                                                                                                                                                17-DEC-1999;
                                                                                                                                                                                                                                                                                   05-JUL-2000
                                                                                                    (AJIN ) AJINOMOTO CO
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                                                      Zakataeva NP,
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99RU-0104431
                                                                                                                                                                                                                                   99EP-0125263.
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                                                      Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                        Aleshin VV,
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Best Local
                                                                                                                                                                  08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the YeaS amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alanine, valine, histidine, isolaucine, glutamic acid and projection of the coling of the coling accurate th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marine melA; selectable marker; oyster larva settlement; pigmentation; melanin; p-hydroxyphenylpyruvate-hydroxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 21;
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N-PSDB; A52689.
  WPI; 1996-039515/04
N-PSDB; T06767.
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                                                                                                                                                                                                                                                                                                                                                                                                           Shewanella colwelliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mel-linked mlgA gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R87527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R87527 standard; Protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterium.
                                                                                                                                                                                                                                                                 21-MAR-1990;
                                                                                                                        (UYMA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLAQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          awagvatlikttpilfnivrylgafyllylgskilyat----lkgknseaksdepgygai 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnyw-tylvgaifivlvpgpntlfvlknsvssgmkggylaacgvf-----igdavlmfl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEWWFAYLLTSIILTLSPGSGAI----NTMTTSLNHGYPAG-GVYCWASDRTGDSYC--A 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fvtqyirtkkklakvgnsliglmfvgfaarlat 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fkralilsltnpkailfyvsffvqfidvnaphtgisffilaatlelvsfcylsfliisga 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLK---SLASTQSRRH--L 110
                                                                        νς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The bacterium used is E. coli.
                                                                        Weiner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                        MARYLAND BALTIMORE
                                                                                                                                                                                      93US-0148945.
90US-0496804.
                                                                                                                                                                     92US-0974837
                                                                                                                                                                                                                                                                 90US-0496804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29pp;
                                                                        RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid exc
                                                                                                                                                                                                                                                                                                                                                                                                             strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 195.5; DB 2
Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                              07-JUN-1995;
21-MAR-1990;
10-NOV-1992;
08-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colvelliana melA gene (T06766), and was designated mlgA (mel-linked gene). The role of the encoded protein (R87527) was unclear as deletion subcloning in E. coli demonstrated that only melA was require
                                                                                                                                                                                                                                                                                                                      Ś
                                       MelA melanin protein e.g. cosmetics
                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                            US5846531-A.
                                                                                                                                                                                                                                                                 Shewanella colwelliana
                                                                                                                                                                                                                                                                                     MlgA; marine bacterium; melanin synthesis; marine exopolysaccharide; UV blocker; sunscreen; MelA.
                                                                                                                                                                                                                                                                                                                                          11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                              W73358;
                                                                                                                                                                                                                                                                                                                                                                                  W73358 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Fig 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oyster settlement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel gene encoding marine melA from Shewanella - useful as selectable marker in genetic engineering and for inducing i
                 Example 7; Fig 13; 57pp; English.
                                                                      N-PSDB; V08553
                                                                                 WPI; 1999-058995/05
                                                                                                                                                                                                                         08-DEC-1998
                                                                                                                          (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for melanogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      138 fsmlayas 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVMIGYAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WRGVGTLFSRSVIA------FEVLKWAGAAYLIWLGIQQWRAAGAI-DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dntssqisnralitqgfvtaianpkgwafmisllppfisvdqaiapqlmvllsiimmtef 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 AA;
                                                                                                       Weiner RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
                                                                                                                                              90US-0496804.
92US-0974837.
93US-0148945.
                                                                                                                                                                                                                                                                                                                  MlgA protein sequence
                                                                                                                                                                                                   95US-0476254.
                                                                                                                                                                               95US-0476254
                                                                                                                                                                                                                                                                                                                                                                                   Protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.68; 29.78;
                                                   from
                                                   marine bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 155; DB
Pred. No. 6.6e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17;
5.6e-10;
tes 51;
                                                   1
                                                  useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for inducing larval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                   ą
                                                   blocker
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This sequence is the Shewanella colwelliana

MlgA protein,

which

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999999999888
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B40407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antitheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism, SCID; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bong demarca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related to the MelA protien of the invention. The invention relates to MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides. The MelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass or in paints and coatings for plastics, synthetic resins and fabrics, rubber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX ORF171 polypeptide sequence SEQ ID NO:342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B40407 standard; Protein; 130 AA.
                                                                                                                                                                                                                                           05-OCT-2000
                                                                                                                                                                                                                                                                              WO200058473-A2
                                                                                                                                                                                                                                                                                                             Homo sapiens
 N-PSDB;
                                                 Shimkets RA,
                                                                                                                                                     31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                         31-MAR-2000; 2000WO-US08621
                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                     30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 fsmlayas 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 IVMIGYAT 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dntssqisnralitqgfvtaianpkgwafmisllppfisvdqaiapqlmvllsiimmtef 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WRGVGTLFSRSVIA------FEVLKWAGAAYLIWLGIQQWRAAGAI-DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \verb|wmmvgelagvalvaiaavmgvasmmlnypqlfdilkwvgglylgyigismwrakgkmanl|
                2000-602362/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reading frame; ORFX; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                contraceptive.
                                                                                                                                                                                                                                                                                                                                                                cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                      2000US-0540763
                                                   Leach M;
                                                                                                                                     99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 155; DB 20;
Pred. No. 6.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; hepatotropic;
nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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XX Novel nucleic acids and peptides derived from open reading frame X, PT useful for treating e.g. cancers, proliferative disorders, PT neurodegenerative disorders and cardiovascular disease - XX claim 11; Page 608; 5507pp; English.

CC 274446 to C77606 encode the proteins given in B40237 to B43397, which CC represent the human ORFX open reading frames 1 to 3161. The ORFX XX cryoscale antiparkinsonian; nootropic; neuroprotective; osteopathic; cardiant; antiparkinsonian; nootropic; neuroprotective; osteopathic; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antibacterial; cc antivaral; antifungal; antirheumatic; antithyroid; and antianaemic. The csequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an CC proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative clisorders, osteoarthritis, graft vs host disease, cardiovascular disease, clistorage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune cc disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cc enhance coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 130 AA;
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Matches
                                                                                                                                                                                         Query Match
                                                                           139 --QQPQLMQYIVLGVTTIVVDIIVMIGYATLAQ--RIALWIKGPKQMKALNKIFGSLFML 194
121 lglnlafaq 129
                        195 VGALLASAR 203
                                                 63 ggtapal-qmlvlsgvfmamtlavfvlygllanvfrrav-vesprvqnwlrrsfatafag
                                                                                                                                 79 AAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMP 138
                                                                                                                                                                            Local
                                                                                                         w
                                                                                                        1 Similarity 40; Conserv
                                                                                                                                                              Conservative
                                                                                                                                                                            13.6%;
31.0%;
                                                                                                                                                               22;
                                                                                                                                                                Score 144; DB 21;
Pred. No. 9.5e-09;
2; Mismatches 61;
                                                                                                                                                                                           Length 130;
                                                                                                                                                                  Indels
                                                                                                                                                                  6;
                                                                                                                                                                  Gaps
                                                                                                               62
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Qy Qy

Qy Db

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SULT 7
1786
B01786 standard; Protein; 223 AA.
B01786;

03-JAN-2001 (first entry)
Escherichia coli YahN amino acid excretion protein.
E. coli; yahN gene; amino acid production; excretion protein gene; amino acid excretion protein.
Escherichia coli.
Escherichia coli.
Ep1016710-A2.
05-JUL-2000.
17-DEC-1999; 99EP-0125263.
30-DEC-1999; 99RU-0124016.
09-MAR-1999; 99RU-0104431.
(AJIN ) AJINOMOTO CO INC.
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BOLTON BE STAN BE STAN
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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the YahN amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of it gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises
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                                                                                                                                                                                                                                                                                                        EP1016710-A2
                                                                                                                                                                                                                                                                                                                                                                                                    E. coli; yfiK gene; amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                        Tokhmakova IL;
                                                Livshits VA,
                                                                                         (AJIN ) AJINOMOTO CO INC
                                                                                                                                       30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                             17-DEC-1999;
                                                                                                                                                                                                                                                             05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli YfiK amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B01788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B01788 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTLEWWFAYLLT---SIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGW 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glitdlsnpqtvlffisifsvtlnaetptwarlmawagivlasiiwrvflsqafslpavr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glfglatlitqceeifslirivggayllwfawcsmrrqstpqmstlqqpisapwyvffrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       itmdplhavyltvglfvitffnpganlfvvvqtslasgrra-gvltglgvalgdafysgl\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ray----grmqrvasrvigai 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IALWIKGPKQMKALNKIFGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVEVNLTNPKSIVFLAALFPQFIMPQQP---QLMQYIVLGVTTIVVDIIVMIGYATLAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R--GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRH--LFQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223
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                                             Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zakataeva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA,
                                                                                                                                       98RU-0124016
99RU-0104431
                                                                                                                                                                                                             99EP-0125263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 126.5; DB 21
Pred. No. 1.9e-06;
8; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakanishi K,
                                           Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                     production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                             Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                          excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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                                             Troshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    copies of its is E. coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
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RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the YfIK amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increase in threonine, histidine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increased comprises protein -
                                                                                                                                                                                                                                                                      A. vitis hypersensitive response elicitor protein,
                                                                                                                                                                                                                                                                                                                   в11637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-414802/36.
N-PSDB; A52690.
New protein from Agrobacterium vitis, useful e.g.
                        N-PSDB;
                                                                                                        06-NOV-1998;
                                                                                                                                                                                                                         stress
                                                                                                                                                                                                                                    Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer;
                                                                                                                                                                                                                                                                                             23-OCT-2000
                                                                                                                                                                                                                                                                                                                                           B11637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 23;
                                                                                                                               05-NOV-1999;
                                                                                                                                                    18-MAY-2000
                                                                                                                                                                           WO200028056-A2
                                                                                                                                                                                                  Agrobacterium vitis
                                                                               (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR------
                       2000-376567/32
)B; A61502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagisfslavidpaavhllswagaayivwla---wkiatsptked--glqakpisfwasf 111
                                                        ТJ,
                                                                                                                                                                                                                                                                                                                                                                                                   laghlfqrlfrqygrqlnivlall
                                                                                                                                                                                                                                                                                                                                                                                                                                                alqfvnvkiilygvtalstfvlp-qtqalswvv-gvsv----llamig--tfgn--vcwa 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVGTLFSRSVI---AFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           afwtytlitamtpgpnnilalssatshgf----
                                                                                                                                                                                                                                                                                                                                                                                                                         KGPKQMKALNKIFGSLFMLVGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVNLTNPKSIVELAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALWI 175
                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                         resistance; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 11.9%;
Similarity 24.5%;
50; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production increasing
                                                          Herlache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195
                                                                                                                                                                                                                                                                                             (first
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                                                                                                      98US-0107387.
                                                                                                                               99WO-US26079
                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29pp; English.
                                                           TC,
                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of L-amino acids by an the expression amount of
                                                                                                                                                                                                                                                                                                                                           229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 126; DB 21;
Pred. No. 1.8e-06;
6; Mismatches 80;
                                                                                                                                                                                                                         plant.
                                                                                                                                                                                                                                                                                                                                                                                                    185
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                                                           H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -rqstrvlagmslgflivmll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 195;
                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                       ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC elicitor proteins. The HR is a rapid, localised necrosis that is

CC associated with the active defence of plants against many pathogens, and

CC occurs when a pathogenic organism interacts with a nonhost plant (i.e.

CC one in which intracellular bacterial growth and disease development do

CC not occur). Like other HR elicitors, the A. vitis elicitor functions in

CC non-host plants by causing a rapid hypersensitive response that results

CC in walling-off and killing of the pathogen. On grape plants, the A. vitis

CC elicitor induces a restricted necrosis of tissues, resulting in the death

CC of plant cells and induction of pathogen resistance. A. vitis HR elicitor

CC proteins, in non-infectious form, are used to treat plants or their seeds

CC of ungart resistance to disease, such as those caused by fund; bacteria

CC control insects, to impart resistance to environmental stresses, e.g.,

CC cold, and to improve nutritional value, e.g., altered oil content. The

CC same effects can be produced by producing transpenic plants or seeds by

CC incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of

CC and eliminate the need for biological control agents or polluting

CC chamicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                    EP1013765-A1
                                                                                                                                                                     E. coli L-threonine resistance protein, RhtC
                                                                                                                                                                                                           08-SEP-2000
                  28-JUN-2000
                                                                                      Escherichia coli,
                                                                                                                      L-homoserine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences B11630-B11688 represent proteins from Agrobacterium vitis which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (A61501-A61524) encoding the A. vitis HR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             а
                                                                                                                                       L-threonine resistance;
                                                                                                                                                                                                                                                                          Y99598 standard; Protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 85-86; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistance to disease or stress to plants,
                                                                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                                                 174 WIKGPKOMKALNKIFGSLFMLVGALLASA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                       134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 AVEVNLTNPKSIVELAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLTSI--ILTLSPGSGAINTMTTSLNHGYPAG-----GVYCWASDRTGDSYCAGWRGV
                                                                                                                                                                                                                                                                                                                                                                rtvvlrrqrlfniligvvlaslgailfta
                                                                                                                                                                                                                                                                                                                                                                                                                                 giltnglnpktsifvislytqfigkdtp-lshqllwglfislshllwfasvstflsnpai 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yamfgiaiiqhifpnildiikfvgaaylvyaglatafskirdvegslvpsdrsmgremmt 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTLFSRSVI-----AFEVLKWAGAAYLIWLGI-QQWRAAGAIDLKSLASTQSRRHLFQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liasitwlavlspgadfamvsrnsflygrksglaasmgiaiacw------fhvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                         (first entry)
                                                                                                                      L-valine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%;
                                                                                                                                   L-threonine synthesis; rhtC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 123.5; DB 1
Pred. No. 4.4e-06;
                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                  221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is involved in production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the L-threonine resistance protein, RhtB, from Escherichia coli. The coding sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding wild-type the process of the content of the corresponding wild be accorded to the correspon
     17-DEC-1999;
                                                           05-JUL-2000
                                                                                                                                                                                                                         E. coli; yggA gene; amino acid production;
amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   в01789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise
                                                                                                              EP1016710-A2
                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                     Escherichia coli YggA amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                           03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B01789 standard; Protein; 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 15-16; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Escherichia bacterium having enhanced L-threonine resistance to enhanced RhtC protein activity, used to produce L-threonine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-homoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; A48443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-homoserine, L-valine and L-leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 ATLAQRIALWIKGPKQMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 RSVIAFEVLKW-----AGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHL-----FQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LTSIILTLSPGSGAINTMTTSLNHGYPAG-----GVYCWASDRTGDSYCAGWRGVGTLFS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rrgyqrlakwidg-----fagalfagfgihliisr 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kglltnlanpkaiiyfgsvfslfvgdnvgttarwgifaliivetlawftvvaslfalpqm 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAVEVNLTNPKSIVFLAALEPQFIMPQQPQLMQYIVLGVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hlii--ekmawlhtlimvggglylcwmgyqmlr--galkkeavsapapqvelaksgrsfl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mvhivalmspgpdfffvsqtavsrsrkeammgvlgitcgv-----mvwagiallgl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-414602/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zakataeva
     99EP-0125263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98RU-0123511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-0125406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%;
21.0%;
                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 122; DB 21;
Pred. No. 5.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aleshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Belareva AV,
                                                                                                                                                                                                                                               excretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                               protein gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIVVDIIVMIGY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tokhmakova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
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RESULT
W37715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the yggA amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                         LysG; LysE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive.
                                                                                                                                                                            C. glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1998;
09-MAR-1999;
                                                                                            DE19548222-A1
                                                                                                                    Corynebacterium glutamicum
                                                                                                                                                                                                     12-MAR-1998
                                                                                                                                                                                                                            W37715
                                                                                                                                                                                                                                                  W37715 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 25; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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(KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AJIN ) AJINOMOTO CO INC
                        22-DEC-1995;
                                             22-DEC-1995;
                                                                     26-JUN-1997
                                                                                                                                                                                                                                                                                                              171
                                                                                                                                                                                                                                                                                                                                     172
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                                                                                                                                                                                                                                                                                                                                                                                    116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                     ALWIKGPKQMKALNKIFGSLFMLVGALLA 200
                                                                                                                                                                                                                                                                                                                                                                                                        gsallmqspwllalvtwggvafilwygfgafktamssnie-lasaevmkqgrwkilatml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAY------LITSIILTLSPGSGAINTMTTSLNHGYPAG-GVYCWASDRTGDSYCAGWRG 59
                                                                                                                                                                                                                                                                                                             aprlrtakagriinlvvgcvmwfialgla 199
                                                                                                                                                                                                                                                                                                                                                            avtwlnphvyldtfvvlgslggq--ldvepk--rwfalg--tisasflwffglallaawl 170
                                                                                                                                                                                                                                                                                                                                                                                EVNLTNP----KSIVELAALEPQEIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                VGTLFSRSVTAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLAST----QSRRHLFQRAV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                     fsyyfgglalgaamilplgpqnafv--mnggirrgyhimiallcaisdlv--licagifg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-414802/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of L-amino acids by an Escherichia bacterium increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                            Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98RU-0124016
99RU-0104431
                      95DE-1048222
                                             95DE-1048222
                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                          E protein (lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%;
                                                                                                                                                                                                                                                  236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 113; DB 21;
Pred. No. 6.2e-05;
6; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakanishi
                                                                                                                                                                                                                                                  AA
                                                                                                                                                                            export protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 211;
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δ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ.
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Y04104
                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
                                                                                                                  28-AUG-1997;
                                                                                                                                                                 JP11069978-A.
                                                                                                                                                                                                                Arthrobacter
                                                                                                                                                                                                                                      Arthrobacter
                                                                                                                                                                                                                                                                                      Y04104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eggeling L,
                                                                                                                                          16-MAR-1999
                                                                                                                                                                                                                                                              10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                      kvea-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                  X19826
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20 Вр 80 DЬ Ş В

В

PARCE XXX

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Increasing microbial production of amino acids, especially by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the LysE protein product, a lysine export protein. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 42; Page 10; 16pp; German.
Levan fructotransferase gene - fructotransferase
                                                                                                              WPI; 1999-247463/21
                                                                                                                                                                    (NIOC ) NIPPON OIL CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arthrobacter nicotinovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y04104 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-333867/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 PKSIVFLAALFPQFIMPQQPQIMQYIVLGVTTIVVDIIVMIGYATLAQRIALWIK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 meifitglllgaslllsigpqnvlvikggikregliavllvclisdvf--lfiagtlgvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LEWWFAYLLTSIILTLSPGSGAINTMTTSL-NHGYPAGGVYCWASDRTGDSYCAGWRGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      llsnaapivldimrwggiayllwfavmaakda--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLEQRAVEVNLTN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nicotinovorans levan fructotransferase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sahm H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nicotinovorans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                             97JP-0232421
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Pred. No. 0.035;
5; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 levan
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                               for
                            recombinant production of levan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fructotransferase
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RESULT 14
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Best Local S
Matches 41
                                         The present sequence represents Arthrobacter nicotinovorans levan fructotransferase. The present invention also describes a method for the preparation of levan fructotransferase in which a transformant is cultured in a medium and levan fructotransferase is collected from the culture. The method can prepare levan fructotransferase in a
                                                                                                                                                                                    Claim 3; Page 8-9; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arthrobacter nicotinovorans levan fructotransferase protein
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                                                                                                                                                                                                                                                        Levan fructotransferase gene - for recombinant production
                                                                                                                                                                                                                                                                                                         WPI; 1999-247463/21
N-PSDB; X19827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQLMQ-YIVLGVTTIVVDIIVMIGYATLAQRI 171
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41; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0232421
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19.3%; Pred. No. 1.1;
ative 34; Mismatches
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  RESULT 15
Y38701
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Best Local Similarity
Matches 41; Conser
             Amino acid sequences Y38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFS) Z11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related, Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1997;
18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
                                                                                                                                                                                                                                Claim 4; Page 252; 524pp; English.
                                                                                                                                                                                                                                                                          Proteins from Neisseria meningitidis diagnosis, treatment and prevention c
                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-327407/27.
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06-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae antigen encoded by partial ORF104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEW---WFA-------YLLTSIILTLSPGSGAINTMTTSLNHG 35
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                                                                                                                                                                                                                                                                                                                                                                                             G, Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      517
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97GB-0023516.
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97GB-0025158.
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19.3%; Pred. No. 1.2;
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Total number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-875-223-8

US-08-448-603A-30

US-09-134-075-30

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US-08-232-537-2
US-09-09-947-2
US-09-09-947-2
US-08-468-812-2
US-08-863-102-4
US-08-863-102-4
US-08-862-141-1
US-08-87-26-214-1
US-08-726-214-1
US-08-726-214-1
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US-08-726-214-1
US-08-726-214-1
US-08-726-214-1
US-08-726-214-1
US-08-726-21-1
US-08-726-307B-3
US-08-752-307B-3
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5474933-4
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patent No. 5474933
Sequence 24, Appl
Patent No. 5432081
Sequence 8, Appli
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
                                                                                                                                         Sequence
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2, Appli
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18, Appli
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LENGTH: 153 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-254-7
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                                                                                                                        Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1400 K STREET NW
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-2477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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34
39
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ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, JAMES A.
NAME: POULOS III, JAMES A.

NAME: POULOS III, JAMES A.

NAME: TAI
                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,714
REFERENCE/DOCKET NUMBER: JA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-0088
TELEPAX: 202 628-8034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,25
FILING DATE: 06-UN-1995
      99
                                             18
                                             WMMVGELAGVALVAIAAVMGVASMMLNYPOLFDILKWVGGLYLGYIGISMWRAKGKMANL 77
    KSLASTQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDI 158
                                                                                                                            38; Conserv
                                                                                                                            Conservative
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29.7%;
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5268463-8
US-08-867-352-21
US-08-867-352-21
US-09-043-937A-4
US-08-368-071-10
US-08-458-181-10
US-08-458-181-12
US-07-959-943-7
US-07-879-617A-12
US-07-879-943-9
US-08-706-936-2
US-08-707-782-298-2
US-08-637-759B-89
US-09-408-71-558-89
US-09-408-700-013B-15
                                                                                                                          21;
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                                                                                                                          Score 155; DB 2;
Pred. No. 1.2e-10;
1; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
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                                                                                                                                                               Length 153;
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Patent No.
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Result No.

Score

Match Query

Length

DB

1098 379 379 380 380 380 380 453 453

18;

Gaps

2;

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428 534 857 857 456 1302 291 291 291 344 898 898

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database

Title: Perfect score:

US-09-466-935-2 1061

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Scoring table:

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US-09-068-195-24
; Sequence 24, Appli
; Patent No. 6140078
; TYPE: PRT; ORGANISM: L. US-09-068-195-24
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                                                                 SEQ ID NO 24
LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                         TITLE OF INVENTION: Salt-Inducible Promoter Derivable from a Lactic Acid TITLE OF INVENTION: Bacterium, and Its Use in a Lacctic Acid Bacterium for INVENTION: Production of Desired Protein
FILE REFERENCE: Sanders-60113/0252227
CURRENT APPLICATION NUMBER: US9/09/068,195B
CURRENT FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: PCT/EP97/04755
EARLIER FILING DATE: 1997-08-20
EARLIER FILING DATE: 1997-08-20
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER FILING DATE: 1997-03-13
EARLIER FILING DATE: 1997-03-13
EARLIER FILING DATE: 1996-09-05
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sanders, Jan W.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Venema, Gerard
APPLICANT: Kok, Jan
                                                                                                               SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ent No. 5474933

APPLICANT: EINER, RONALD M.; FUOUA JR., WILLIAM TITLE OF INVENTION: MARINE MELA GENE NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 FSMLAYAS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 IVMIGYAT 166
|: ||:
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nes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 974,837
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: 496,804
FILING DATE: 21-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 DNTSSQISNRALITQGFVTAIANPKGWAFMISLLPPFISVDQAIAPQLMVLLSIIMMTEF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 WRGVGTLFSRSVIA------FEVLKWAGAAYLIWLGIQQWRAAGAI-DL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 153
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                        lactis MG1363
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Pred. No. 1.2e-10;
""cmatches 51;
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RESULT 4
5/32081-9
; Patent No. 5432081
; APPLICANT: JEFFERSON, RICHARD A.
; TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E.COLI
;GLUCORONIDE PERMEASE GENE
                                                                                      RESULT 5
US-08-875-223-8
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FILING DATE: 10-NOV-1987
SEQ ID NO:9:
Sequence 8, Application US/08875223
Patent No. 6127175
GENERAL INFORMATION:
APPLICANT: VIGNE, Emmanuelle
APPLICANT: PERRICAUDET, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 447,976
FILING DATE: 08-DEC-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10 CURRENT APPLICATION DATA:
                                                                                                                                                                 188 YFICFKSTRENVVRIVAQPSLNISLQTLKRNRPLFMLCIGAL
                                                                                                                                                                                                     164 Y----ATLAQRIALWIKGPKQMKALNKIFGS--LFML-VGAL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 VSTLVVFVSFILAY 207
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FILING DATE: 15-OCT-1993
                                                                                                                                                                                                                                                                                                                     73 LLFGTAPLMIFSVLVFWVLTDWSHGSKVVYAYLTYMGLGLCYSLVNIPYGSLATAMTQQP 132
                                                                                                                                                                                                                                                                                                                                                                                           14 FAFAMGALFL-LSYYTDVAGVGAAARAHAVTGAGIRCLRRRLCRTSGGQCEYRWGKFRPF 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 FLLLGGLLWFLPVALCAAEMATV--EGWKNGGIFSWVSQTLGERF-----GFAAIFFQWF 90
                                                                                                                                                                                                                                                                                                                                                                                                                      7 FAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASD--RTGDSYCA-GWR----- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 YLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGVGTLFSR--
                                                                                                                                                                                                                                                                        QSRRHL-FQRAVEVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIG 163
                                                                                                                                                                                                                                          QSRARLGAARGIAASLT----FVCLAFLIGPSIKNSSPEEM-VSVYHFXTIVLAIAGMVL 187
                                                                                                                                                                                                                                                                                                                                                     ---GVGTLFSRSVIAFEVL-KWAGA-----AYLIWLGIQQWRAAGAIDLKSLAST----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTQRTAKLVKAGFVVGIVIPSVILFGLAAAY--FIGGNPIEIPINSHAFVPDFSQ-----
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58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /08/138,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Mismatches 101; Indels
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Pred. No. 3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 428;
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APPLICANT:

PERRICAUDET, Michel DEDIEU, Jean-Francois

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US-08-448-603A-30; Sequence 30, Application US/08448603A; Patent No. 5864027
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Best Local S
  GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
APPLICANT: Nakamura, Gerald R
APPLICANT: Nakamura, HIV Envel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNET/AGENT INFORMATION:
NAME: Fehlner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FR 95/00747
FILING DATE: 20-CAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06532
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PROST, Edouard
TITLE OF INVENTION: CELLS FOR THE
TITLE OF INVENTION: ADENOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/10541
FILING DATE: 08-5EP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                     346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 19-JAN
                                                                                                                                                                                                                           84 WLGIQQWRAAGAIDLKSLASTQSRRHLEQRAVEVNLTNPKSIVFLAALF 132
                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/875,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                   IDIMTSMMIHGYESWALHCHCSS-PGSLQCIAGGQVLASWF-RMVV-----DGAMF--
                                                                                                                                                                                                                                                                                                       INTMTTSLNHGYPAGGVYCWASDRTGDSYC-AGWRGVGTLESRSVIAFEVLKWAGAAYLI 83
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500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 amino acids
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VENTION: CELLS FOR THE PRODUCTION OF RECOMBINANT
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23.9%; pred. No. 11.
--ive 21; Mismatches
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HIV Envelope Polypeptides
                      Gerald R.
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                                                                                                                                                                                                    Sequence 30, Application US/09134075 Patent No. 6042836
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                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
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LENGTH: 857 amino acids
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APPLICATION NUMBER: 08/0:
FILING DATE: 07-JUN-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                         APPLICANT: Berman, Phillip W.
APPLICANT: Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                        123 KSIVFLAA------LFPQFIMPQ------QPQLMQYIVLGVTTIVVDIIVMIG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 IEPL------GVAPTKAKRRVVQREKRAVGIGAVFLGFLGA 526
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                                                                                                                                                                                                                                                                                                                587 YLRDQQLLGIWGCSGKLICTTSVPWNASWSNKSLDKIWDNM 627
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             CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/448,603A FILING DATE: 07-JUN-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-393-2286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
COUNTRY: USA
                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                     AGSTMGAASITLTVQARLLLSGIVQQQNNLLRAIEAQQHLLQLIVWGIKQLQARVLAVER 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEVIKWAGAAYLIWIGIQQWRAAGAIDLKSLASTQSRRHLFQR-----AVFVNLTNP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                 E: McCutchen, Doyle, Brown & Enersen, LLP 3 Embarcadero Center
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19.5%; Pred. No. 19;
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RESULT 5432081-7
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5432081-7
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                                                                                                                                                                                                                                                                         ; APPLICANT: JEFFERSON, RICHARD A.
; TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E.COLI
;GLUCORONIDE PERMEASE GENE
                                  SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
                                                   NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/13/
FILING DATE: 15-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 447,976
FILING DATE: 08-DEC-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1989
APPLICATION NUMBER: 119,102
FILING DATE: 10-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 857 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
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NAME: Haliday, Emily
REGISTRATION NUMBER: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   587 YLRDQQLLGIWGCSGKLICTTSVPWNASWSNKSLDKIWDNM 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  492 IEPL----
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                   LENGTH: 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LTSIILTLSPGSGAINTMTTSLNHGYPAGGYYCWASDRTGDSYCAGWRGVGTLFSRSVIA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 6.5%; Score 68.5; I Similarity 19.5%; Pred. No. 19; 43; Conservative 28; Mismatches
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                                                                                                                     Query Match
Best Local Similarity 18.6
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Best Local Similarity 26.1%;
Matches 58; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Peery,
APPLICANT: Skatru
                                                                                                                                                                                                                                                                                                                                                                   NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X921
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
TELEPAX: 317-276-1917
                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 317-276-1917
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Peery, Robert B.

APPLICANT: Skatrud, Paul L.

TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF TITLE OF INVENTION: AUREOBASIDIUM PULLULANS NUMBER OF SEQUENCES: 4

CORPERSONMENTS STATES OF SECURITY STATES OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1302 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                          811 MQWFSGQSVPSLMSSLSSDAGQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 QSRARLGAARGIAASLT----FVCLAFLIGPSIKNSSPEEM-VSVYHFWTIVLAIAGMVL 195
                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 LLFGTAPLMIFSVLVFWVLTDWSHGSKVVYAYLTYMGLGLCYSLVNIPYGSLATAMTQQP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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                                                                                            3 LEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGVGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 FAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASD--RTGDSYCA-GWR----- 58
                     LF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GVGTLFSRSVIAFEVL-KWAGA-----AYLIWLGIQQWRAAGAIDLKSLAST----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFICFKSTRENVVRIVAQPSLNISLQTLKRNRPLFMLCIGAL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSRRHL-FQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAFAMGALFL-LSYYTDVAGVGAAARAHAVTGAGIRCLRRRLCRTSGGQCEYRWGKFRPF 80
                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indiana
---SRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSR-RHLFQRAV 115
                                                                                                                                                                                                                                                                                                            1302 amino acids
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                                                                                                                                                       18.6%;
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                                                                                                                                                       Score 67.5;
Pred. No. 45;
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Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  X9212
                                                                                                                                      Mismatches
                                                                                                                                                                      DB 1; Length 1302;
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                                                          --- ACLSGVAIGT 843
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                                                                                                                                    Gaps
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US-08-358-171-2
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TELEX: 248633

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FENGTH: 291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5763578
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-28-5197
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 IVMIGYAT--LAQRIALWIKGPKQMKALNKIFGSL--FMLVGALLASARHA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              844 IFTVCVSITGGIILAHVVAWKIAVVLL-AAVPVMITAGYVRLRVLALAESRHRSAYNDAA 902
                                                                                                                       104 ---TQSRRHLFQRAVEVNLTNPKSIVFLAALEPQFIMPQQPQLMQYIVLG-----VTTI 154
                 215 LPARTLLLGWGPYALLYLYATIADATSISPKLQMVPALIAKAVPTVNAMNYALGS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 16-DEC-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        11 LTSIILTLSPGSGAINTM---TTSLNHGYPAGGVYCWASDRTGDSYCAGWRG----VGTL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                              CSSAAVAWGRYHHFCTRSRLDWNTAVSLVFFVWLSSAFWAALPLLGWGHYDYEPLGTCCT 163
                                                                                                                                                                                               FSRSVIAF-----EVLKWAGA---AYLIWLGIQQWRAA----GAIDLKSLAS--- 103
                                                                                                                                                                                                                                      LLVLSLALADSGISLNALVAATSSLLRRWPYGSEGCQAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLALSFSITYFVYALAYW-WGAKQVR--NGTYSQLDFFIVLPALLFSAQSA 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVT------TIVVDI 158
                                                  VVDIIVMIG-----YATLAQRI-----ALWIKGPKQMKALNKIFGS 190
                                                                                      LDYSRGDRN-FTSFLF-----TMAFFNFLLPLFITVVSYRLMEQ-KLGKTSRPPVNTV
                                                                                                                                                                                                                                                                                                           ch 6.3%; score 66.5; similarity 21.7%; pred. No. 7 51; Conservative 35; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FONG, Henry K.W.
FONG, Henry K.W.
VENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
VENTION: ENCODING SAME, AND ANTIBODIES THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                               76;
                                                                                                                                                                                                                                                                                                                                              Length 291;
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                                                                                                                                                                                                                                    --GFQGFVTALASI 103
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APPLICANT:
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US-09-090-947-2
Sequence 2, Application US/09090947
Patent No. 6008338
GENERAL INFORMATION:
                                                           RESULT 12
US-08-468-812-2
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Sequence 2, Application US/08468812 Patent No. 5935836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                            155 VYDIIVMIG-----YATLAQRI-----ALWIKGPKQMKALNKIFGS 190
                                                                                                                                                                                                                                                                                           104 CSSAAVAWGRYHHFCTRSRLDWNTAVSLVFFVWLSSAFWAALPLLGWGHYDYEPLGTCCT 163
                                                                                                                                     215 LPARTLLLGWGPYALLYLYATIADATSISPKLQMVPALIAKAVPTVNAMNYALGS
                                                                                                                                                                                                                 164 LDYSRGDRN-FTSFLF-----TMAFFNFLLPLFITVVSYRLMEQ-KLGKTSRPPVNTV
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                                                                                                                                                                                                                                                                                                                                                                                                          11 LTSIILTLSPGSGAINTM ~- ~ TTSLNHGYPAGGVYCWASDRTGDSYCAGWRG -- ~ + VGTL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/090,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                  ---TQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLG-----VTTI 154
                                                                                                                                                                                                                                                                                                                                FSRSVIAF-----EVLKWAGA---AYLIWLGIQQWRAA-----GAIDLKSLAS---
                                                                                                                                                                                                                                                                                                                                                                       LLVLSLALADSGISLNALVAATSSLLRRWPYGSEGCQAH------GFQGFVTALASI 103
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)GY: linear
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%;
21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66.5; DB 3;
Pred. No. 7.4;
5; Mismatches 76;
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Vehmaanper , Jari

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RESULT 13
US-08-863-102-1
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                                                                                                      Sequence 1, Application US/08863102 Patent No. 6015828
                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
                                                                     GENERAL INFORMATION: APPLICANT: Cuppol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 29-UUL-11
CLASSIFICATION: 435
CLASSIFICATION: 435
             APPLICANT: Cuppoletti, John
TITLE OF INVENTION: Chemical Modification of
TITLE OF INVENTION: Chloride Channels as a Treatr
TITLE OF INVENTION: Fiobrosis and Other Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bugaisky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-771-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/332,412
FILING DATE: 31-OCT-1994
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NUMBER OF SEQUENCES:
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CITY: Washington
                                                                                                                                                                                                              88 GNEVAGKGWSTGGRRTVTYNASENPSGNGYLTLYGWTRNPLVEYYIVESW 137
                                                                                                                                                                                                                                                 61 GTLFS------RSVIAFEVLKWAGAAYLIWLG-----IQQW 90
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                                                                                                                                                                                                                                                                                                                         10 LLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASD-----RTGDSYCAGWRGV 60
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Lahtinen, Tarja
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Fagerstr m, Richard
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Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                  Treatment
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RESULT 14
US-08-863-102-4
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                                                                                                           GENERAL INFORMATION:
APPLICANT: Cuppoletti, John
TITLE OF INVENTION: Chemical I
TITLE OF INVENTION: Chloride
TITLE OF INVENTION: Fiobrosis
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 47; Conser
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
TYPE: amino acid
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APPLICATION NUMBER: US/08/863,102
FILING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: ZUICher, J. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 977-8377
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COMPUTER READABLE FORM:
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ADDRESSEE: Jackie A. Zurcher,
ADDRESSEE: Dinsmore & Shohl LLP
STREET: 255 E. Fifth Street,
STREET: 1900 Chemed Center
CITY: Cincinnati
STATE: Ohio
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ADDRESSEE: Dinsmore & Shohl LLP
STREET: 255 E. Fifth Street,
STREET: 1900 Chemed Center
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.1
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25.0%;
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Pred. No. 35;
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Diskette, 3.5 inch

COUNTRY:

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Best Local Similarity 25.0
Matches 47; Conservative
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Patent No. 5773009
GENERAL INFORMATION:
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ODERATING SYSTEM: MS-DOS
SOFTWARE: WORDPETECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,102
FILLING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: ZUICHET, J. A.
REGISTRATION NUMBER: 42,251
REGISTRATION NUMBER: 42,251
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INFORMATION FOR SEQ ID NO: 4:
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APPLICANT:
APPLICANT:
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LENGTH: 898 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
                                                                                                                                                                                                                                            TITLE OF INVENTION: ROTAVIRUS STRAIN AND RELATED TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                             30303
                                                                                                                                                  Atlanta
                                                                                                               Georgia
Y: USA
                                                                                                                                                                                                                                                                                 GLASS, ROGER I.
GENTSCH, JOHN R.
BHAN, M. K.
DAS, BIMAL K.
                                                                                                                                                                     127 Peachtree Street, Suite 1200
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Pred. No. 35;
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; MOLECULE TYPE: protein US-08-802-141-4
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
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APPLICATION NUMBER: 08/231,04

FILING DATE: 15-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.

REGISTRATION UNBER: 36,016

REFERENCE/DOCKET NUMBER: 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 404/688-0770
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APPLICATION NUMBER: US/08/802,141
FILING DATE: 19-FEB-1997
CLASSIFICATION: 424
                                                                                                                                                                                            102 WMFTYL---VLPNTAQTSVVVNVMNETVN------ISIDNSGSAY------ 137
                                                                                                                                138 -KFVDYFKT---
                                                            180 SDAYGDLRVGTYFNPVPNAVINLNADF--YVIPDSQQEMCTEYIRRGLPAIQTTTYVTPI
                                                                                                 122 -----
238 SYAVRSQRIA 247
                               163 GYATLAQRIA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 40%,
TELEPHONE: 40%,
TOTAL: 688-9880
                                                                                                                                                           65 SRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLTN--- 121
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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8

Search completed: May Job time: 414 sec 6, 2001, 14:39:23 ì

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9b_bal:AE004372

9b_bal:AE004786

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9b_htg25:LMFLCHR32_2

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Query length: 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -Q=/cgn2_1/USPTO_spool/US09466935/runat_03052001_075709_14798/app_query.fasta_1.529
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-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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346820 i AP003008 Mesorhizobium loti
296950 i AP003008 Mesorhizobium loti
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14807 i AB024601 Pseudomonas aerugino
110000 i Continuation (21 of 28) of
720 i AR063272 Sequence 6 from patent
885 i X67020 S.colwelliana mlgA gene.
96231 i AF188935 Bacillus anthracis p
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1231 : AX030175 S
91414 ! M87049 E.
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                                                                                       31 | AXXXXXII Sequence 1 from Pater 414 | M877049 E. coli genomic sequence 1 | M877049 E. coli genomic sequence 1 | AXXXXII Sequence 1 | AXXXXII Sequence 1 | AXXXII Sequence 1 | AXXII Sequence 1 | AXXXII Se
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AUTHORS
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US-09-466-935-2 x AX030175
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84 rpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSer
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gb_pat1:AX030175
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AX030175
AX030175.1 GI:10190392
                                                                                                                                                                                                                                                                                                                      Gene and method for producing 1-amino acids Patent: EP 1013765-A 1 28-JUN-2000;
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Belareva, A.V., Aleshin, V.V., Livshits, V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; gamma subdivision; Enterobacteriaceae;
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i NAE004079 Xylella fastidios
i U04992 Pseudomonas aerugino
i U81259 Pseudomonas aerugino
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Quality: 1061.00 Ratio: 5.176 Percent Similarity: 100.000 Percent Identity: Length: Gaps: 205 0 100.000

1 MetThrLeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuTh 17

606

from: 1 to: 1231

17 rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnH 34 GCTGTCGCCAGGCTCTGGTGCAATCAACACTATGACCACCTCGCTCAACC 656

34 isGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGly ACGGTTATCCGGCCGGTGGCGTCTATTGCTGGGCTTCAGACCGGACTGGC 50

AspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSe 67 GATTCATATTGTGCTGGTTGGCGTGGGGTTGGGACGCTATTTTCCCGCTC

rValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleT 84 806

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REFERENCE
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                                                 AUTHORS
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Direct Submission
Submitted (12-FEB-1992) Donna L. Daniels, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoll@genetics.wisc.edu; Phone: 608-262-2534; Fax:
                                                                                                                                                                                                                                                                                                                2 (bases 1 to 91414)
Plunkett,G. III., Burland,V., Daniels,D.L. and Blattner,F.R. Analysis of the Escherichia coli genome. III. DNA sequence cregion from 87.2 to 89.2 minutes
Nucleic Acids Res. 21 (15), 3391-3398 (1993)
                                                                                                95184296
                                                                                                        A new family of peptidyl-prolyl isomerases Trends Biochem. Sci. 20 (1), 12-14 (1995)
                                                                                                                                            Rudd, K.E., So
Rouviere, P.E.
                                                                                                                                                                                                  Analysis of the Escherichia coli genome. IV. region from 89.2 to 92.8 minutes Nucleic Acids Res. 21 (23), 5408-5417 (1993)
                                                                                                                                                                                                                                                                  Blattner, F.R., Burland, V., Plunkett, G. III.,
                                                                                                                                                                                                                                                                                                                                                                                                               Science 257 (5071),
                                                                                                                                                                                                                                                                                                                                                                                                                            Daniels,D.L., Plunkett,G. III., Burland, Analysis of the Escherichia coli genome: from 84.5 to 86.5 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli genomic sequence
M87049
                                                               Daniels, D.L
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1 (bases 1 to 91414)
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608-263-7459
On May 29, 1995 this sequence version replaced gi:148169.
This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. The entire sequence was independently determined from E. coli MG1665. Overlaps and conflicts with other sequence determinations are annotated. Reference [1] describes the original sequence determination of a 91408 bp sequence. References [2], [3], and [4] describe subsequent corrections and/or updates to that

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V00349 (164.

of 81 degrees"

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77

degrees"

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CDS gene promoter promoter

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misc_feature
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3458. .3556
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RSPHHASSLTAMVGGGAIPGPGEISLAHNGVLFLDELPEFERGTLDALREPIESGQIH
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1223. .:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted bend of 79 3297. .3326
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LEIPLPPPGILSKTVVPGESSATVKQRVMAARERQFKRQNKLNAWLDSPEIRQFCKLE
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                                                                                                               inactive
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                                                                                                               coli K12"
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                                                                                                                                                                                                                                                                                                                                                                                                  61861 GCTGGCCTCTACTCAATCGCGTCGACATTTGTTCCAGCGCGCAGTTTTTG
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                                                                                                                                    167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isGlyTyr.ProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGl
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RHEQGAAMAAIGYARATGKTGVCIATSGPGATNLITGLADALLDSIPVVAITGQVSAP
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1039.00 5.093 99.029 Percent Length:

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CDS

gene

62011 CGATTCATATTGTGCTGGGTTGGGGGTTGGGACGCTATTTTCCCGCT yAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgS 67 61962

61961 CAGTGATTGCGTTTGAAGTGTTGAAGTGGGCAGGCGCGCCTTACTTGATT erValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIle 83 61912

61911 TGGCTGGGAATCCAGCAGTGGCGCCGCCGCTGGTGCAATTGACCTTAAATC rLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPheV 117 61862

61762

61812

gene

CDS

gene

CAATTCATCATGCCGCAACAGCCGCAACTGATGCAGTATATCGTGCTCGG GlnPheIleMetProGlnGlnProGlnLeuMetGlnTyrIleValLeuGl 61712

61711 CGTCACCACTATTGTGGTCGATATTATTGTGATGATCGGTTACGCCACCC yValThrThrIleValValAspIleIleValMetIleGlyTyrAlaThrL 61662 167

LeuAsnLysIlePheGlySerLeuPheMetLeuValGlyAlaLeuLeuAl 200 euAlaGlnArgIleAlaLeuTrpIleLysGlyProLysGlnMetLysAla 183 TTGCTCAACGGATTGCTCTATGGATTAAAGGACCAAAGCAGATGAAGGCG 61612

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REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                 AL Submitted (13 - OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA On Sep 9, 1997 this sequence version replaced 9:1790254. This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants H600301 and H601428 (from the Human Genome Project and NGHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: markeamber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World wide Web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aSerAlaArgHisAla
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                                              (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                       Genome Project's World Wide Web site
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3 (bases 1
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                          them to be searched for in Entrez as gene
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/note="0122; sequence change shortens and
/note="0122; sequence change shortens and
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                          changesN-terminus
SW: P27846)"
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1077. .:
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                                                                                                                                                                         /note="b3823"
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/transl_table=11
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/EC_number="3.6.1.-"
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RPEYAALGQLARQRF9TIPFMALTATADDTTRQDIVRLLGLNDFLIQISSEDRNIRYN
LMEKEKPLDQLMRYVQEQRGKSGIIYCNSRAKVEDTAARLQSKGISAAAYHAGLENNV
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PAEAKLFYDPADMAWLERCLEEKPQGQUQDIERHKLANAGAFAEAQTCRRLVTLLNYFG
EGROEPCGNCDICLDPR(XYDOSTDAQIALST)IGRVKORFGMGYVVPEV IRGANNQATE
DYGHDKLKVYGMGRDKSHEHWVSVIRQLIHLGLVTQNIAQHSALQLTEAARPVLAESS
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GPNSVLGASYTQKSWWQLSNSEESSPFRETNYEPQLFLGFATDYRFAGWTLRDVEMGY
NHDSNGRSDPTSRSWNRLYTRLMAENGNWLVEVKPWYVVGNTDDNPDITKYMGYYQLK
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/function="enzyme; Central intermediary metabolism:
/hosphorus compounds"
/note="0289; 99 pct identical to PA1_ECOLI SW: P00631;
                                                                                                                                                                                                                                                                                                                                                                          /note="factor Sigma70; predicted +1 start at 4005588"
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alignment_block:
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MetThrLeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuTh 17
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                                                                                                                                                                                                                        Ratio:
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                                                      reverse of:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="factor: 5426. .545"
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4384. .5406
/gene="p1dB"
/EC_number="3.1.1.5"
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4384..5
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/note="factor Sigma70;
5438. .5466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="1ysophospholipase L(2)"
/protein_id="AAC76828.1"
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/db_xref="GI:2367303"
/db_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorus compounds"
/note="0340; 99 pct identical amino acid sequence and equal length to PLDB_ECOLI SW: P07000"
/codon_start=1
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Qravevnltneksivelaalfeqeimeqqpqlmqyivlgvttivvdiivmigyatlaq
Rialwikgekqmkalnkifgslemlvgallasarha"
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/db_xref="GI:2367302"
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IIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKW
IDGFAGALFAGFGIHLIISR"
                                                                                                                                                                                                                                                                                                                               /note="factor Sigma70;
5526. .6041
/gene="yigL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRSTEV"
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complement(4227. .4254)
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/function="orf; Unknown"
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/note="b3824"
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seq_documentation_block:
LOCUS AE005613
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                        Escherichia coli 0157:H7.
Escherichia coli 0157:H7
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Escherichia coli 0157:H7
AE005613 AE005174
AE005613.1 GI:12518685
Genome sequence of enterohemorrhagic Escherichia coli O157:H7 Nature 409 (6819), 529-533 (2001) 2 (bases 1 to 10592)
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complement(72. .836)
/gene="Z5332"
complement(72. .836)
/gene="Z5332"
                                                                                                                                                                                                                                                                                                                                                                                                     product="mg2+ transport, system I"
protein_id="naces009.1"
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VIMEGHQGDEYDEALSTLAELEDIGWKYRLCLMDTQRALNFTVRKARLPGGQLEQARE
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ILRDIESLLPHMESLFQXVNFLMQAAMGFINIEQNRIIKIFSVVSVVFLPPTLVASSY
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                                                                                                                                                                                                                          complement(2198. .2689)
/gene="Z5334"
                                                                                                                                                                                                                                                                        complement(2198. .2689)
/gene="z5334"
                                                                                                                                                                                                                                                                                                                 /note="0-island #156; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                                                                                                                                                                  GMNFEFMPELKWSFGYPGAIIFMILAGLAPYLYFKRKNWL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strain MG1655: B3816" /codon start-
                                                                            /protein_id="AAG59010.1"
/db_xref="GI:12518688"
                                                                                                                                                                       /function="orf; Unknown functi
/note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="orf; Unknown function"
note="Residues 1 to 131 of 254 are 95.41
residues 1 to 131 of 161 from Escherichia
                                                                                                                               /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="corA"
/note="z5333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MG1655: B3815"
                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="transport; Transport of small molecules:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="corA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /serotype="0157:H7"
/db_xref="taxon:83334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1206. .2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="0-island #155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Escherichia coli 0157:H7"
/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plunkett, G. III, Burland, V.,
                                                                                                                                                                                                                                                                                                                                                                              .4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #155; Region of the EDL933 chromosome not coli K-12 MG1655"
                                                                                                                                                                                                   tunction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mau,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glasner, J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pct identical to coli K-12 Strain
                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Z5339"
4483. .4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3748. .3867
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3748. .3867
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                                                                                                                                                                                       complement(4841. .5728)
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/gene="rarD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3892. .4278)
/gene="z5337"
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                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4483. .4794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="orf; Unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="orf; Unknown function"
/note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2686. .3534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2686.
/gene="Z5335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="25335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                   .5728)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corA"
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magnesium transport protein (CORA) (SP:P31138) [Salmonella
typhimurium LT2]"
/note="Residues 4 to 295 of 295 are 92.12 pct identical to residues 8 to 299 of 300 from Escherichia coli K-12 Strain MG1655: B3819"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNFEFMPELKWSFGYPGAIIFMILAGLAPYLYFKRKNWL"
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alignment_block:
US-09-466-935-2 x AE005613/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AE005613 from: 1
                                                                                                                                                                                                                                                                            10441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10541 TGCAATCAACACTATGACCACCTCGCTCAACCACGGTTATCGCGGGGGGG 10492
                                                                                           10341
                                                                                                                                                                                     10391
                                                                                                                                                                                                                                                                                                                                                                       10491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                         72 uValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnG
                                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 yAlaIleAsnThrMetThrThrSerLeuAsnHisGlyTyrProAla..Gl
                                                                                                                                                                                     AGTGTTGAAGTGGGCAGGCGCGGCTTACTTGATTTGGCTGGGAATACAGC 10342
                                                                                                                                                                                                                                                                            GTTGGCGTGGGGTTGGGGACGCTATTTTCCCGCTCAGTGATTGCGTTTGA 10392
                                                                                                                                                                                                                                                                                                   lyTrpArgGlyVal.GlyThrLeuPheSerArgSerValIleAlaPheGl 72
                                                                                                                                                                                                                                                                                                                                                                  TGGCGTCTATTGCCGGGCTTCAGACCGGACTGGCGATTCATATTGTGCTG 10442
yGlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="pldA"
/note="Z5342"
6412...7281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1780..6265)
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/function="orf; Unknown function"
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to residues 1 to 161 of 161 from Escherichia coli K-12
strain MG1655: B3820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mdakotrogevlialaaayeimglapakeklikyvpadeilihhrvi
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agivytypllcetraaatheklstlgffgyigptlmfllavifygekpgadkmytftfi
wvalaifyndaiytorrks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="enzyme; Central intermediary metabolism: Phosphorus compounds"
/note="residues 1 to 289 of 289 are 100.00 pct idento residues 1 to 289 of 289 from Escherichia coli K Strain M61655: B3821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="orf, hypothetical protein"
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FAQLAFKNQPMMVGNWAQSILHGGVIASALRAGNKVAVARVELHNEEQLYIASATATYMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5780. .6265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       950.00
4.847
97.512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5412. .7281
/gene="pldA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 2
Percent Identity: 96.517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 are 100.00 pct identical from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 10592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10542
  10242
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS STYSTMD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10041 GCTCGTTGTTTATGCTGGTGGGAGCGCTGTTAGCATCGGCGARGCATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10091 TCTATGGATTAAAGGACCAAAGCAGATGAAGGCGCTGAATAAGATTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10241 CAAAAGTATTGTGTTTCTGGCGGCGCTATTTCCGCAATTCATCATGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10141 GTCGATATTATTGTGATGATCGGTTACGCCACCCTTGCTCAACGGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 ValaspileileValmetileGlyTyralaThrieuAlaGlnArgileAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 lySerLeuPheMetLeuValGlyAlaLeuLeuAlaSerAlaArgHisAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
    rRNA
                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_ba3:STYSTMD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium LT2.
Salmonella typhimurium LT2
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                           coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs GLIMMER (Salzberg, S., Delcher, A., Kasif, A. and White, O. (1998) NAR 26,544-548), and GeneMark (Lukashim, A.V. and Borodovsky, M. (1998), NAR 26,1107-1115.
                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 96086)
Washington University Genome Sequencing Center.
The Salmonelia typhimurium Genome Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF233324
AF233324.1 GI:6960215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STYSTMD1 96086 bp DNA Salmonella typhimurium fragment STMD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-FEB-2000) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 96086)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella.
                                                                                                                                                                                                                                                                           NOTES:
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/strain="SGSC1412"
/db_xref="taxon:99287"
/clone="STMD1"
<1. 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center
Department of Genetics, Washington Ur
St. Louis, MO 63110, USA
e-mail: sclifton@watson.wustl.edu or
jspieth@watson.wustl.edu
                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dq 98096
                                                                                                           .96086
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Missouri 63108, USA
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complement(1506. .2354)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="tRNA-Trp"
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													<del></del>					ĄĘ		AUTHORS TITLE JOURNAL		ACCESSION VERSION KEYWORDS SOURCE ORGANISM
of 936 l unknown of 142 l		* 12322 12652; CONTUG OF 331 DP IN TENGUN * 12653 14116; CONTUG OF 1464 DP IN LENGTH  * 12653 14116; CONTUG OF 1464 DP IN LENGTH  * 12322 12652; CONTUG OF 1464 DP IN LENGTH  * 12322 12652; CONTUG OF 331 DP IN LENGTH  * 12322 12652; CONTUG OF 331 DP IN LENGTH  * 12322 12652; CONTUG OF 331 DP IN LENGTH  * 12322 12652; CONTUG OF 331 DP IN LENGTH  * 12322 12652; CONTUG OF 331 DP IN LENGTH  * 12522 12652; CONTUG OF 331 DP IN LENGTH  * 12652 12652; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG OF 331 DP IN LENGTH  * 12652 14165; CONTUG OF 331 DP IN LENGTH  * 12652 14165; CONTUG OF 331 DP IN LENGTH  * 12653 14165; CONTUG	gap of unknown lengt 12321: contig of 817 bp in gap of unknown lengt	gap of unknown lengt 11504: contig of 660 bp in	of 822 k unknown of 608 k	* /640 8442: CONTIG OF 803 DD IN length  * 8443 9414: CONTIG OF 972 DD IN length  * GAB Of UNKNOWN length	gap of unknown lengt 7639: contig of 876 bp in gap of unknown lengt	* 5572 5967: contig of 396 bp in length  * 5572 gap of unknown length  * 5968 6763. contig of 796 bp in length	gap of unknown lengt 5571: contig of 793 bp in	91. 19 19 19	gap of unknown lengt 3686: contig of 987 bp in gap of unknown lengt	ш ти		1 752: 753 1000:	* However, it should not be assumed that this clone * will be sequenced to completion. In the event that * the record is updated, the accession number will * be preserved.	* and the order in which they appear is completely  * arbitrary. Low-pass sequence sampling is useful for  * identifying clones that may be gene-rich and allows  * overlap relationships among clones to be deduced.	* NOTE: This record contains 198 individual  * NOTE: This record contains 198 individual  * sequencing reads that have not been assembled into  * contigs. Runs of N are used to separate the reads	Submitted (10-JAN-2000) Production Sequencing Pacility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 17 2000 this sequence version replaced dis686488.	2 (bases 1 to 256373) DOE Joint Genome Institute. Direct Submission	DOE Joint Genome Institute. Sequencing of Mouse Unpublished	Eukaryota; Mammalia;	AC020870 AC020870, 2 GI:6984372 HTG: HTGS_PHASEO. house mouse. Mus musculus

19242 20454

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33 nHisGlyTyrProAlaGlyGl             :::	17 rLeuSerProGlySerGlyAl 	1 MetThrLeugluTrpTrpPheAl 	Align seg $1/1$ to reverse of: A	alignment_block: US-09-466-935-2 x AC020870/rev	alignment_scores: Quality: 795.00 Quality: 795.00 Ratio: 4.789 Percent Similarity: 95.402 F	* 67041 67560: *	* 66042 67040:	* 65591 66041:	* 65367 65590:	* 65077 65366:	* 64040 65076:	* 63594 64039:	* 62714 63593:	* 62639 62713:	* 61763 62638:	* 61085 61762:	* 60827 61084:	* 59907 60826:	* 59084 59906;	* 58530 <b>5908</b> 3:	* 58320 58529:	* 57673 58319:	* 56935 57672:	* 56359 56934:	* 55471 56358:	* 54634 55470:	* 53366 54633:	* 52700 53365:	* 51829 52699:	* 50849 51828:	* 50305 50848;
.GlyGlyValTyrCysTrpAlaSerAspArgTh 49	rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAs 33 :	MetThrreugluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuTh 17 	AC020870 from: 1 to: 256373	:	Length: 174 Gaps: 3 Percent Identity: 93.678	of 520 unknow	e of	Of 5	of		2 5	of a	of 88	of 75 b	of 87	contig of 678 bp in length	gap of unknown length contig of 258 bp in length	contig of 920 bp in length	of 823 bp in	of		of u		gap or unknown length contig of 576 bp in length	tig of 888 b	contig of 837 b	contig of 1268	contig of 666 b	contig of 871 b	contig of 980	contig

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31202: 32688: 33431:

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25957: 27260: 27266: 28596: 29473: 30372:

34616:

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TITLE
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AUTHORS
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                                 * NOTE: This record contains 8 individual

* sequencing reads that have not been assembled into

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be generich and allows

* overlap relationships among clones to be deduced.

* However, It should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome SAMPLING.
                                                                                                                                                                                                                                                                                                                                  Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 4833)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4833)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                        Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                           Center: Joint Genome Institute Center Code: JGI
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  836: contig of
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836 bp in length
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                                                                                  AACTGATGCAGTATAGTCGTGGCTCGGGCCGGTCGAGCGCAGGCGTAGGT
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contig of 109 bp in length
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contig of 23 bp in length
gap of unknown length
contig of 223 bp in length
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contig of 1204 bp in length
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sign of 1204 bp in length
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sed_nome: 19_InG/:RCU2U9//U  sed_accumentation_block: DEFINITION  MS muscullis close RP23-252M21, WORKING DRAFT SEQUENCE, 144  ACCESSION  MS muscullis close RP23-252M21, WORKING DRAFT SEQUENCE, 144  ACCESSION  MS muscullis close RP23-252M21, WORKING DRAFT SEQUENCE, 144  ACCESSION  MS muscullis close RP23-252M21, WORKING DRAFT SEQUENCE, 144  ACCESSION  MS muscullis close RP23-252M21  MS muscullis Close RP23-252M	0-0 3-4 . 0
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KEYWORDS
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ACCESSION
VERSION
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LOCUS AC0208
  REFERENCE
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US-09-466-935-2 x AC020970/rev
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 265383)
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HTG; HTGS_PHASE0.
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	COMMENT	JOURNAL	TITLE	REFERENCE	AUTHORS TITLE
sequencing record contains 244 individual contigs. Runs of N are used to separate the reads and the order in which they appear is completely intitizing. Low-pass sequence sampling is useful for intitizing longs that may be generich and allows located relationes beauting of 889 bp in length be reserved.  870 1188: contig of 889 bp in length gen of unknown length 1182 2002: contig of 1021 bp in length gen of unknown length 2561 3646: contig of 759 bp in length gen of unknown length 4521 4813 can of 1021 bp in length gen of unknown length 4521 4813 contig of 686 bp in length gen of unknown length 4521 4813 contig of 687 bp in length gen of unknown length 6601 6992: contig of 874 bp in length 6601 6992: contig of 875 bp in length 6601 6992: contig of 680 bp in length 6601 6992: contig of 681 bp in length 6601 6992: contig of 681 bp in length 6601 6992: contig of 682 bp in length 6602 contig of 683 bp in length 6603 end of unknown length 6603 end of unknown length 6604 end of unknown length 6605 end of unknown length 6606 end of unknown length 6607 end of unknown length 6608 end of unknown length 6609 end of unknown length 6600 end of unknown length 6600 end of unknown length 6600 end of unknown length 6601 end of unknown length 6602 end of unknown length 6603 end of unknown length 6603 end of unknown length 6604 end of unknown length 6605 end of unknown length 6606 end of unknown length 6607 end of unknown length 6608 end of unknown length 6609 end of unknown le	2800 Mitchell Drive, Walnut Creek, CA is sequence version replaced gi:668643	ted (10-J) Institut	nstitute.	unpublished  ( bases 1 to 265383)  The Taint Group Institute	DOE Joint Genome Institute. Sequencing of Mouse
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q of 998 bp in length
of unknown length
g of 1329 bp in length
f unknown length
g of 462 bp in length
of unknown length
g of 133 bp in length
g of 834 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g of 384 bp in length funknown length g of 229 bp in length it unknown length funknown length g of 652 bp in length
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Gaps: 6
Identity: 60.426
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g of 355 bp in l
f unknown length
g of 769 bp in l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HONO Sapiens chromosome SAMPLING.
              * NOTE: This record contains 175 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                         Submitted (23-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primate
1 (bases 1 to 170178)
DOE Joint Genome Institute.
                                                                                                                                                                                                                               Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASEO.
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DOE Joint Genome Institute.
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However, it should not be assumed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
    clone
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* 18076 18233: contig of 158 bp in length  * 18076 ap of unknown length	of 80 br	of 233 b	of 154 b	of 654 b	of 291 b	of 67 bp	<ul> <li>15975 16596: contig of 622 bp in length</li> <li>agap of unknown length</li> </ul>	<ul> <li>15216 15974: contig of 759 bp in length</li> <li>gap of unknown length</li> </ul>	<ul> <li>* 15037 15215: contig of 179 bp in length</li> <li>* qap of unknown length</li> </ul>	<ul> <li>* 14183 15036: contig of 854 bp in length</li> <li>* gap of unknown length</li> </ul>	* 13628 14182: contig of 555 bp in length  * qap of unknown length	* 12949 13627: contig of 679 bp in length  * gap of unknown length	of 657 k unknown	of 1023 unknown	of 818 b unknown	of 315 b unknown	of 936 bp in unknown lengt	9199: contig of 117 bp in gap of unknown lengt	of 1028 bp ir unknown lengt	8054: contig gap of	7879: contig of 314 bp in gap of unknown lengt	of 650 bp in unknown lengt	of 704 bp in unknown lengt	of 651 bp in unknown lengt	* 4876 5560: contig of 685 bp in length  * gap of unknown length	1 2 2	of 500 b	of 586 k	of 648 b	tig of 181 b	of 700 b	of 614 k	of 707 unknow	635: contig of 635 bp in gap of unknown lengt	l, the accession nu	ompletion. In
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36331	35601	35490	34745	33856	33124	32507	31734	31681	31511	31275	30694	30238	29144	28932	28762	27579	26913	26718	26072	25795	24821	24451	23550	23193	23018	22417	21070	20116	20018	19866	19706	19491	19300	19077	18937	18234
gap of unknown lengt contig of 214 bp in	gap of unknown lengt contig of 730 bp in	gap of unknown lengt contig of 111 bp in	gap of unknown lengt contig of 745 bp in	gap of unknown length 34744: contig of 889 bp in length			gap of unknown length 32506; contig of 773 bp in length	31733: contig of 53 bp in length	31680: contig of 170 by in length	gap of unknown length 31510: contig of 236 bp in length	gap of unknown length 31274: contig of 581 bp in length	unknown of 456	gap of unknown length 30237: contig of 1094 bp in length	unknown of 212 b	28931: contig of 170 bp in length	of 1183	of 666 b	of 195 b	gap of unknown tength 26717: contig of 646 bp th		1 2 5	24820: contig of 370 bp in length	25		0	gap of unknown len	gap of unknown lengt contig of 1347 bp in	gap of unknown leng	<pre>gap of unknown length 20115: contig of 98 bp in length</pre>	$\overline{}$	unknown of 160 b	$\sigma$	tig of 191 b	of unknown	19076: contig of 140 bp in length	of Lig

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alignment_scores:
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                       AlaAlaLeuPheProGlnPhe 135
                                                                                             CGAGACGGCTGCCACCTCTTCGCCACGCAGACTAATATCC....
                                                                                                           sSerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValP 116
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                                                                                                                                             TATTCTGATTGTGGTTGTGCGACGTAATGCCCCGGCCCGACGCATTGCAA 20057
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                                                                                                                                                                                                                                                                                                                                             ACGGTTATCGCGGCGCGGTGGCGTCTATTGCTGGGCTTCAGACCGGACTG
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Gaps:
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contig of 166 bp in le
gap of unknown length
contig of 674 bp in le
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of 659 bp
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of 616 bp in length
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of 856 bp in length
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of 689 bp in length
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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LOCUS AE004104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.I. Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragol, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medical Center Dr, Rockville,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-JUN-2000) The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio
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RQIGHYHEFQUYNDWYLRPWALLITQIMAAVTLKPSYAPGYGPYHAKPFHLNLLTHSETR
                                                                                                                                                                                                                                                                                                           complement(1014. .2030)
/gene="VC0135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="VC0134"
complement(72. .899)
/gene="VC0134"
/note="identified by Glimmer2;
                                                                                                                                                                                                                                                           similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                     complement(1014. .2030)
                                                                                                                                                                                                                                                                                                                                                                                                              DQDHEHLVQYETLLNQRFGDKLNVAFSTPWCLEVMCAGVSKGDALQAVAESLHLGLEN
CIAFGDGMNDVEMLSMAGKGLVMGTAHEKVFNALPDNEVIGSNADDAVAHYLHQHLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKHDKQLEVHLYRNDEWMLNKEDEILRDFHEDSGFTYRVFDVNNAPTDGIAKIFFTQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="biotype:
complement(72.
                                                                                                                                                                                                                                                                                                                                                             /gene="VC0135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFIFATGRHHIDVAGIREIAGIPAYMITSNGARVHDQNDQLMYSKNVPQDLVQAIIDV
                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                             /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="N16961"
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                                                                                                                                                                                                                                                                                   note="similar to PID:1449198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MTTSAHKHPYKIVASDLDGTLLAPNHQLSEFSKQTLKQLHDKGF"
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2105. 2722
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complement(4148. .4618)
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2670. .3968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:L42023 SP:P45173 PID:1007363 PID:1221482 PID:1205585; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3976 .4095)
/gene="VC0138"
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VMFGYTALAAQLGRYIRSPNIMTRMNKLEGSMEMGCGMLLATAKA"
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US-09-466-935-2 x AE004104
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      17
                                                                ATGGATATCCATGTTTGGCTTGCCTATCTACTGACCGCGGTGGTGTTTAG
rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnH 34
                                                                                                 MetThrLeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuTh 17
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5322 .5690
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3
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Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T.  Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  JOURNAL Nature 406 (6799), 959-964 (2000)  MEDLINE 20437337  REFERENCE 2 (bases 1 to 10475)  AUTHORS Stover, C.K., Pham, X. Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J.,	Pseudomonas aeruginosa.  Pseudomonas aeruginosa  Bacteria; Proteobacteria; gamma subdivision; P Pseudomonas.  1 (bases 1 to 10475)  Stover, C. K., Pham, X. Q., Erwin, A. L., Mizoguchi, Hickey, M. J., Brinkman, F. S., Hufnagle, W. O., Kow Garber, R. L., Colltry, L., Tolentino, E., Westbroc Brody, L. L., Coulter, S. N., Folger, K. R., Kas, A., Brody, L. L., Coulter, S. N., Folger, K. R., Kas, A.,		euAlaSe	165 laThr LeuklaGlokrg HeAladeutrp Helys GlyproLys GlnMet 181	PheProGlnPheIleMetProGlnGlnProGlnLeuMetGlnTyrIleVa	2351 TTAGTATGGCTGGGTATTCAGAAATGGCGAGATAGAGCCCCCTAACGGC 2400  98 uLysSerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaV 115 :::	:   :::            ::::::   :::::   ::::
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gene

gene

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LMLQAGPAGHNAVIGGAATAVVLLIGLAWVILRGSAKLPLGLFFSINAALLCALSVVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6887. .8803)
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   CTGCTGGCGCAATACCTGATCATGGGCGCCACCATGATCGTCGTCGACCT
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GlnLeuMetGlnTyrTleValLeuGlyValThrThrTleValValAspIl 158
                                     TGATCTTCATGCTCGCGGTGCTGCCGCAGTTCATCGACCCGCACCAGCCG
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                                                                                                           GACCCTGGTGCTGGTTTCCTGGTCAACGCCAGCAATCCCAAGGCGG
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                                                                                                                                                                                ...CCACAGGCCTTGAGCACCGATGGCGAACGGCCTCTGGGGGCGACCGTT 4986
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* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.  * overlap relationships among clones to be deduced.  * will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.  * 1014 1615: contig of 1013 bp in length app of unknown length app of unk	158 elleValmetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpI 175  1835 GATCGTCAGCCGGCTACACCGGGCTGCCGCGCGTACCGCGTAC 4786  175 LeLyGGlyProLyGGlnMetLysAlaLeuAsnLysIlePheGlySerLeu 191  175 1cLyGGlyProLyGGlnMetLysAlaLeuAsnLysIlePheGlySerLeu 191  176 177 1cLyGGlyProLyGGlnMetLysAlaLeuAsnLysIlePheGlySerLeu 191  177 177 177 177 177 177 177 177 177 1
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contig of 1073 bp in length
gap of unknown length
contig of 243 bp in length
gap of unknown length
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contig of 720 bp in length
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contig of 1592 bp in length
gap of unknown length
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contig of 949 bp in
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g of 1005 bp in length
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g of 446 bp in length
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alignment\_scores:

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397.50

Length:

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REFERENCE
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                SOURCE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block: LOCUS AC020833
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Percent Similarity:
                                                                                                                   AUTHORS
TITLE
                                                                                                   JOURNAL
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Direct Submission

Submitted (10-JAN-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA * NOTE: This record contains 69 individual

* sequencing reads that have not been assembled into * sequencing reads that have not separate the reads * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 62274)
DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                        2 (bases 1 to 62274)
DOE Joint Genome Institute.
                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                  AC020833.1 GI:6686475
HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                                                                                                                    house mouse.
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Percent Identity: 64.052
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94598, USA
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gap of unknown length 21500 21570: contig of 71 bp in length gap of unknown length	unknown lengt of 719 bp in	of 568 bp in	unknown lengt of 719 bp in	unknown lengt of 778 bp in	gap of unknown lengt contig of 777 bp in	gap of unknown lengt contig of 777 bp in	unknown lengt of 735 bp in	unknown lengt of 688 bp in	unknown lengt of 869 bp in		unknown lengt of 148 bp in		of 453 k	of 982 k	of 805 b	of 618 bp in	of 594 bp in	<pre>* 9059 9678: contig of 620 bp in length</pre>	* gap of unknown length * 8254 9058: contig of 805 bp in length	unknown lengt of 687 bp in	unknown lengt of 713 bp in	unknown lengt of 399 bp in	unknown lengt of 870 bp in	unknown lengt of 288 bp in	unknown of 530	unknown lengt of 1121 bp ir	unknown of 692	* 2421 2953: contig of 533 bp in length	* 1813 2420: contig of miles the length  * 1813 2420: contig of miles the length	of 763 b	<ul> <li>297 1049: contig of 753 bp in length</li> <li>gap of unknown length</li> </ul>	gap of unk	* be preserved.  * 1 296: contin of 296 hm in length	<pre>* will be sequenced to completion. In the event that * the record is updated, the accession number will</pre>	* overlap relationships among clones to be deduced. * However, it should not be assumed that this clone	* identifying clones that may be gene-rich and allows
FEATURES source												-											_						•							
* 59221 L 1	* 56785 *	* 53729 *	* 51662 *	* 49872 *	* 48116	* 47109	* 45675	* 4436	* 4325	* 42388 *	* 40875 *	* 39841 *	* 3885	* 38148 *	* 37014 *	* 35822 *	* 34993 *	* 34311 *	* 33043 *	* 32934 *	* 32153 *	* 31515 *	* 30781	* 29992 *	* 29003	* 28058	* 27153 *	* 26269 *	* 25821	* 2508/	יא ל מת	* 24651	* 23944	* 22941 *	* 22379	* 21571 *
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BASE COUNT
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AUTHORS
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Ratio:
                              Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti DNA Res. 7, 331-38 (2000)
                                                                                  Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto, Watanabe,A., Idesawa,K., Ishikawa,K., Kawashima,K., Kimura,T., Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuno,A., Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M., Takeuchi,C., Yamada,M. and Tabata,S.
Kaneko, T.
                                                                                                                                                                                                                               Mesorhizobium loti
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                                                                                                                                                                                           Phyllobacteriaceae; Mesorhizobium.
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                  GACGGAACCGCT...AGGAAGCCGCGCGGCGCCTTCTTCCTGCAGGGCCT
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AGCTCATGTCCAGGATCAGCGGCAGCTTCTTGGTCGGTGGCGGCCTGTGG
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Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:kaneko@kazusa.or.jp.
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Fax:81-438-52-3934)
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                                                                                                                                                                Sequence 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 10-11;
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/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:V52660
Novel RhtB protein, useful for generation of L-homoserine resistance Escherichia bacteria and large-scale production of e.g. L-homoserine
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                                                                                                                                                                      13-OCT-1998;
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KW L-threenine; L-valin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-466-935-2 x Z94405
                                                                                                                                                                        seq_name:
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                                                      E. coli L-homoserine
                                                                                                                                 A48442 standard; DNA; 1231
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                                                                                                                                                                                                                                                 uAlaGlnArgIleAlaLeuTrpIleLysGlyProLysGlnMetLysAlaL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTCATATTGTGCTGGTTGGCGTGGGGTTGGGACGCTATTTTCCCGCTC
                                                                                                                                                                                                 TCGGCGAGGCATGCG 1171
                                                                                                                                                                                                                SerAlaArgHisAla 205
                                                                                                                                                                                                                                                                                                                                                        GTCACCACTATTGTGGTCGATATTATTGTGATGATCGGTTACGCCACCCT
                                                                                                                                                                                                                                                                                                                                                                      ValThrThrIleValValAspIleIleValMetIleGlyTyrAlaThrLe
                                                                                                                                                                                                                                                                                                                                                                                                          AATTCATCATGCCGCAACAGCCGCAACTGATGCAGTATATCGTGCTCGGC
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                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A48442
               resistance; L-homoserine synthesis; L-valine; L-leucine; ds.
                                                                               (first entry)
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                                                    resistance gene, rhtB
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alignment_block:
US-09-466-935-2 x A48442
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                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: A48442 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the L-homoserine resistance gene, rhtB, from Escherichia coli. This sequence may be used to impart L-homoserine resistance on E. coli bacteria, which would be useful for producing a high yield of L-homoserine. L-homoserine resistance means that the bacteria will be able to grow on a minimal medium containing L-homoserine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-homoserine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-threonine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Escherichia bacterium having enhanced L-threonine resistato enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
                                                                707
                                                                                                                             657
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                                                                                                                                                                                          607 GCTGTCGCCAGGCTCTGGTGCAATCAACACTATGACCACCTCGCTCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1231 BP; 291 A; 319 C; 311 G; 310 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 12-13; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Livshits VA,
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AspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSe
                                                                                                                                          isGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGly
                                                                                                                                                                                                                                                       ATGACCTTAGAATGGTGGTTTGCCTACCTGCTGACATCGATCATTTTAAC
                                                                GATTCATATTGTGCTGGTTGGCGTGGGGTTGGGACGCTATTTTCCCCGCTC
                                                                                                                             ACGGTTATCCGGCCGGTGGCGTCTATTGCTGGGCTTCAGACCGGACTGGC
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DB; Y99597.
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Ratio: 5.176
milarity: 100.000
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seq_documentation_block:
ID A52689 standard: DNA,
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AC A52689;
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AC A52689;
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DT 03-JAN-2001 (first (
XX)
DT 03-JAN-2001 (girst (
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Escherichia coli.
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KW E. coli; yeas gene; (
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Escherichia coli.
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CDS 11.6
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FT CDS
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                                 Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
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DB; B01787.
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99RU-0104431
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/product= "Yeas"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the yeas gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alanine, histidine, isolaucine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                      389
                                                                                                                                                                                                                                                                                            124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 639 BP; 142 A; 128 C; 161 G; 208 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 19-20; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 CTGAATTACTGG...ACCTATCTGGTTGGGGCCATTTTTATTGTGTTGGT
                                                                                                                                                                                                         ProGlnLeu...MetGlnTyrIleValLeuGlyValThrThrIleValVa
                                                                                                                                                                                                                                                    CCATTTTGTTCTATGTGTCGTTTTTCGTACAGTTTATCGATGTTAATGCC
                                                                                                                                                                                                                                                                                            erileValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln 140
                                                                                                                                                                                                                                                                                                                                                                             s....LeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAla 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTAATTAAGACCACCCCGATATTATTCAACATTGTACGTTATCTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euAsnHisGlyTyrProAlaGly...GlyValTyrCysTrpAlaSerAsp
:::::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rProGlySerGlyAlaIle......AsnThrMetThrThrSerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLeuSe
AGTACATACGTACCAAAAAGAAACTGGCTAAAGTTGGCAACTCACTGATT
                                                                                                                           lAspIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaL
                                                                                                                                                                                                                                                                                                                                     CGGTGCTATTTTTAAACGCGCGTTAATTTTGAGCCTGACTAATCCGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                        .....CTGAAGGGTAAAAATAGCGAGGCCAAATCCGATGAGCCCCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleAspLeuLys.....SerLeuAlaSerThrGlnSerArgArgHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTTTATTTGCTCTATCTGGGGAGTAAAATTCTTTACGCGACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...ATTGGCGATGCGGTATTGATGTTTCTGGCATGGGCTGGAGTGGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgThrGlyAspSerTyrCys.....AlaGlyTrpArgGlyValGlyTh
                                      euTrpIleLysGlyProLysGlnMet...LysAlaLeuAsnLysIlePhe
                                                                                GAGTTTCTGCTATTTGAGCTTCCTGATTATATCTGGTGCTTTTGTCACGC
                                                                                                                                                                      CCACATACGGGAATTTCATTCTTATTCTGGCGGCGACGCTGGAACTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rLeuPheSerArgSerValIleAlaPheGluValLeuLysTrpAlaGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAAAGGCGGTTATCTTGCGGCCTGCGGTGTATTT.....
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1.387
66.197
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Gaps:
Percent Identity:
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10
28.638
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GlySerLeuPheMetLeuValGlyAlaLeuLeuAlaSer

GGTTTGATGTTCGTGGGTTTCGCTGCCCGACTGGCGACG

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alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                                                                                                               alignment_block:
US-09-466-935-2 x T06767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID T06767 standard; DNA; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:T06767
                                                                                            Align seg 1/1 to: T06767
                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                                                                                                                                    The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colwelliana melA gene (T06766), and was designated mlgA (mel-linked gene). The role of the encoded protein (R87577) was unclear as deletion subcloning in E. coli demonstrated that only melA was require
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RBS
                                                                                                                                                                                                                                               Sequence 720 BP; 180 A; 165
                                                                                                                                                                                                                                                                                                                                                                                               Novel gene encoding marine melA from Shewanella - useful as selectable marker in genetic engineering and for inducing larval oyster settlement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-039515/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fuqua WC, Weiner RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5474933-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shewanella colwelliana strain LSTDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mlgA gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marine melA; selectable marker; oyster larva settlement; pigmentation; melanin; p-hydroxyphenylpyruvate-hydroxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mel-linked mlgA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T06767;
                                      122 TTTTTACCGACCTTTTTTTCGTCTCAATTACACCAGGTATGTGTATGAC 171
                                                                                                                                                                                                                                                                                                                                                                      Example 7; Fig 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; R87527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1995
                                                                                                                                                                                                                                                                        tor melanogenesis.
25 eAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGlyGlyValT 42
• :::;||||| ::::::: |||
                                                               TyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0148945.
90US-0496804.
92US-0974837.
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                                                                                                                                                             184.00
1.546
56.667
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                                                                                            from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                             Percent Identity: 27.619
                                                                                                                                                                                                                                               C;
                                                                                                                                                                                                                                              165 G; 210 T; 0 other;
                                                                                           to: 720
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seq_documentation_block:
ID V08533 standard; DN
                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:V08533
                                                                                                                                                                                                                                                                                                                                                     V08533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      673 TTAATGATCTGTGTTGGCTTATGGTTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374
 07-JUN-1995;
                              07-JUN-1995;
                                                                08-DEC-1998
                                                                                                US5846531-A
                                                                                                                                                                                                 Shewanella colwelliana.
                                                                                                                                                                                                                                MlgA; marine bacterium; melanin synthesis; marine exopolysaccharide; UV blocker; sunscreen; MelA; ss.
                                                                                                                                                                                                                                                                                colwelliana MlgA coding sequence
                                                                                                                                                                                                                                                                                                                  11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                   V08533 standard; DNA; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AATGGGTCGGTCGGCTCTATCTTGGTTACATCGGCATTAGCATGTGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 GGGTGTCGCCAGTATGATGCTGAACTATCCACAACTCTTCGATATTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 ACTGGCCATGACTCTCGGTATGAGTATCGGTGTG.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 AlaAlaGlyAlaIle...AspLeuLysSerLeuAlaSerThrGlnSerAr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GlyValGlyThrLeuPheSerArgSerValIleAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValValAs 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGAGCGCTAATAACTCAAGGCTTTGTCACCGCAATTGCTAATCCAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuPheMetLeuValGlyAlaLeuLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCTTCAGCATGCTTGCCTATGCGAGCGG.CGGAAAACCCCTTAAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGTTGGTGAGCTAGCAGGCGTTGCCCTCGTGGCGATTGCCGCCGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGATTGCACCACAATTAATGGTATTACTGTCAATTATTATGATGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGGGCCTTTATGATCTCGCTGCTCCCCCCTTTTATCAGCGTTGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erIleValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAAAGGGAAAATGGCCAACCTTGACAATACCTCCAGTCAGATCAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpIleLysGlyProLysGlnMetLysAlaLeuAsnLysIlePheGlySer 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaGlyTrpArg
                                                                                                                                                                                                                                                                                                                  (first entry)
95US-0476254.
                                95US-0476254
                                                                                                                                               Location/Qualifiers 167..628
                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                     ВP
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alignment_block:
US-09-466-935-2 x V08533
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides. The MelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass on in paints and coatings for plastics, synthetic resins and fabrics, rubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g.
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                                                                                                                                                                                           324
                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encoues the amendment of the invention relates to related to the MelA protien of the invention. The invention relates to related to the MelA protien of the genus Shewanella, Vibrio or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 13; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MelA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fuqua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-1990;
10-NOV-1992;
                                                                                                                 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 TTTTTACCGACCTTTTTTTCGTCTCAATTACACCAGGTATGTGTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYMA-) UNIV MARYLAND
                                     424
                                                                         107
124
                                                                                                                                                   92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                               AlaAlaGlyAlaIle...AspLeuLysSerLeuAlaSerThrGlnSerAr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaIl
                                                                                                                                                                                         AATGGGTCGGTGGGCTCTATCTTGGTTACATCGGCATTAGCATGTGGCGG
                                                                                                                                                                                                               ysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArg
                                                                                                                                                                                                                                                                                                                                                ATGGTTGGTGAGCTAGCAGGCGTTGCCCTCGTGGCGATTGCCGCCGTAAT
                                                                                                                                                                                                                                                                                                                                                                                    GlyValGlyThrLeuPheSerArgSerValIleAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGGCCATGACTCTCGGTATGAGTATCGGTGTG........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGlyGlyValT
erIleValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln
                                     TCGAGCGCTAATAACTCAAGGCTTTGTCACCGCAATTGCTAATCCAAAAG
                                                                           gArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS
                                                                                                                 GCCAAAGGGAAAATGGCCAACCTTGACAATACCTCCAGTCAGATCAGTAA
                                                                                                                                                                                                                                                                    GGGTGTCGCCAGTATGATGCTGAACTATCCACAACTCTTCGATATTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaGlyTrpArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence encodes the Shewanella colwelliana MlgA protein, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanin protein from marine bacteria -
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92US-0974837.
93US-0148945.
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Gaps:
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seq_documentation_block: ID C74616 standard: cD
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
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C74446 to C77606 encode the proteins given in B40237 to B43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antianaemic; gene therapy; cancer; proliferative disorder; hyperte neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulant; thrombolytic; coagulant; vasotropic; antidiabeti hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirematic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
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                                                                   Claim
                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis;
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                                                                     <u>ن</u>
                                                                                                                                                                                                                                                               CURAGEN CORP
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                                                                                                                                                                                                                                                                                              99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cartilage damage; contraceptive; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS;
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vulnerary;

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seq_documentation_block:
ID A52688 standard; DNA,
XX
AC A52688;
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DT 03-JAN-2001 (first e
XX
DE Escherichia coli yahn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAl
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                                                                                                                                                                                                                                                                                                                  CTTTGCCGGGCTGGGGTTGAACCTGGCGTTTGCGCAG 387
                                                                                                                                                                                                                                                                                                                                                                        uPheMetLeuValGlyAlaLeuLeuAlaSerAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGAGTCGCCACGTGTGCAGAACTGGCTGCGACGCAGTTTTGCCACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .CAGATGCTGGTACTGAGCGGCGTGTTCATGGCGATGACGCTTGCAG
   coli yahN gene
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144.00
1.694
65.891
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                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 31.008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
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alignment_block:
US-09-466-935-2 x A52688
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                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Livshits VA, z.
                                                                                             134
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the yahN gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                         181
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 672 BP; 130 A; 154 C; 178 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 17-18; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli; yahN gene; amino acid production; excretion protein gene;
amino acid excretion protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1999;
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rLeuPheSerArgSerValI1eAlaPheGluValLeuLysTrpAlaGlyA
                                                                                                                                                GATTACTTTTTTAATCCGGGAGCCAATCTCTTTGTGGTAGTACAAACCA
                                      GCCTGGCTTCCGGTCGACGCGCA...GGGGTGCTGACCGGGCTGGGCGTG
                                                                                                                    erLeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAsp
                                                                                                                                                                                                   ATCACTATGGATCCTTTGCATGCCGTTTACCTGACCGTAGGACTGTTCGT
                                                               ArgThrGlyAspSerTyrCysAlaGlyTrpArg.....GlyValGlyTh
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DB; B01786.
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99RU-0104431
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1.037
60.697
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1..672
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/product= "YahN"
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Gaps:
Percent Identity:
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52690
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A52690 standard; DNA; 588
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09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli yfiK gene
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Increased production of L-amino acids by
                                WPI; 2000-414802/36
P-PSDB; B01788.
                                                                                TOkhmakova IL;
                                                                                              Livshits VA,
                                                                                                                           (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                    coli; yfik gene; amino acid production;
ino acid excretion protein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCAAATGAGCACCACTACAACCAACCGATTAGCGCCCCCTGGTATGTCTT
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::||||||||:::|||::::::
GCGCTTATCTCTTATGGTTTGCGTGGTGCAGCATGCGCCGCCAGTCAACA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHis.....Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTAATTACGCAGTGTGAGGAGATTTTTTCGCTTATCAGAATCGTCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpIleLysGlyProLysGlnMetLysAlaLeuAsnLysIlePheGlySer 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACGTTTAATGGCCTGGGCGGGGATTGTGCTCGCATCAATTATCTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                       coli.
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                                                                                              Zakataeva
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                                                                                                                                                          98RU-0124016
99RU-0104431
                                                                                                                                                                                                           99EP-0125263
                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "Yfik"
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                                                                                               NP,
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                                                                                              Nakanishi
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 an
                                                                                                                                                                                                                                                                                                                                                                                                                                  excretion protein
                                                                                              Aleshin VV,
 Escherichia bacterium
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                                                                                              Troshin
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                               PV;
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alignment_scores
                                                                                                                                                                                                                The present sequence is the yfik gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in threonine, histidine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises increasing the expression amount of an L-amino acid protein \boldsymbol{\cdot}
                                                                                                                                Sequence 588 BP; 113 A; 134 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 22; 29pp; English.
                                                                                                                                167 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          excretion
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Quality: Ratio: Percent Similarity: US-09-466-935-2 x A52690 126.00 1.125 54.902 from: Percent Identity: 6 24.510 204

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Align seg 1/1 to: A52690
                                                                                                                                                                                     421 TGGGTAGTT...GGCGTCAGCGTT.....TTGCTGGCGATGAT
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494 ATCTGTTTCAGCGATTGTTTCGCCAGTATGGTCGCCAGTTAAATATCGTG
                                          179 ysGlnMetLysAlaLeuAsnLysIlePheGlySerLeuPheMetLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 CCAACAAAGGAAGAC.....GGACTTCAGGCAAAACCAATCAGCTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 GCTTTTTGGACTTACACCCTGATTACCGCTATGACGCCAGGACCGAACAA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaTyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                        nArgAlaValPheValAsnLeuThrAsnProLysSerIleValPheLeuA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTCTGGGATTTTTGATTGTGATGTTACTGTGTGCGGGCATTTCATTTTC
                                                                                                                                  eGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpIleLysGlyProL
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                                                                                                                                                                                                                                TyrIleValLeuGlyValThrThrIleValValAspIleIleValMetIl 162
                                                                                                                                                                                                                                                                               TTACGGCACTGTCGACGTTTGTTCTGCCG...CAAACACAGGCGTTAAGC
                                                                                                                                                                                                                                                                                                                                                                             GGCCAGCTTTGCTTTGCAGTTTGTGAACGTCAAAATCATTTTGTACGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGCCAGTGATTGACCCCGCCAGCGGTACACCTTTTGAGTTGGGCGGGGG
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GlyAlaLeuLeu

199

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seq_documentation_block:
ID A61501 standard: DNA:
AC A61501;
XX A61501;
XX A61501;
XX AFFER A. vitis hypersensiti
XX Hypersensitive respon
XX AGROBACTETIUM vitis.
PN W020028056-A2.
XX AGROBACTETIUM vitis.
PN W020028056-A2.
XX BURNAY-2000.
XX Hemany-2000.
XX Hemany-2000.
XX Hemany-2000-376567/32.
PR P-PSDB; B11630, B1163
XX Hew protein from Agro
PR P-PSDB; B11630, B1163
XX Hew protein from Agro
PT resistance to disease
PT A hypersensitive respon
XX Hew protein from Agro
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XX Hew protein from Agro
PT resistance to disease
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XX Hew protein from Agro
PT resistance to disease
PT A hypersensitive respon
XX Sequences A61501-A61:
Agrobacterium vitis by Comp in which intracely
CC cone in which intracely
CC control insects and to end
CC control insects and to end
CC control insects and to end
CC control insects, to:
CC control of previously
CC and eliminate the new
CC control and eliminate the new
CC chemicals.
XX
                                                             alignment_scores:
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                                                                                                                                                                                                                                                         CC Agrobacterium vitis hypersensitivity response (HR) elicitor proteins (C (B11630-B11688). The HR is a rapid, localised necrosis that is C (B11630-B11688). The HR is a rapid, localised necrosis that is C associated with the active defence of plants against many pathogens, and CC occurs when a pathogenic organism interacts with a nonhost plant (i.e. CC one in which intracellular bacterial growth and disease development do CC not occur). Like other HR elicitors, the A. vitis elicitor functions in cC in mailing-off and killing of the pathogen. On grape plants, the A. vitis clicitor functions of plants by causing a rapid hypersensitive response that results (C in mailing-off and killing of the pathogen. On grape plants, the A. vitis clicitor corrections in non-host plants by causing a rapid hypersensitive response that results (C in plant cells and induction of pathogen resistance. A. vitis HR elicitor croteins, in non-infectious form, are used to treat plants or their seeds (C inspart resistance to disease, such as those caused by fund; bacteria (C control insects, to impart resistance to environmental stresses, e.g., cc cold, and to improve nutritional value, e.g., altered oil content. The C control insects, to impart resistance to environmental stresses, e.g., cc cold, and to improve nutritional value, e.g., altered oil content. The C control of previously untreatable diseases, provide systemic treatment; and end for historical contents acents crocliving the may allow (C control of previously untreatable diseases, provide systemic treatment; and content the need for historical content.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 82; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORR ) CORNELL RES FOUND INC.
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   Quality:
Ratio:
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1.056
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                                                                                                                                                  441 A;
                                                                                                                                                                                                                                         for biological control
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Length:
Gaps:
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                                                                                                                                                  342
                                                                                                                                                  Η;
                                                                                                                                                  0 other;
                                                                                                                                                                                                                                         agents or
209
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seq_documentation_block:
ID A61502 standard; DNA;
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US-09-466-935-2 x A61501/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: A61501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                    138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         535
               Hypersensitive response elicitor protein; HR; d insecticide; fungicide; antiviral; bactericide;
                                                                        A. vitis hypersensitive response elicitor-encoding DNA, SEQ ID NO:11
                                                                                                              23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                       194 LeuValGlyAlaLeuLeuAlaSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                           177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 CTGATTGCTTCGATAACCTGGCTGGCCGTTCTCAGCCCCGGCGCGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 uPheGlnArgAlaValPheValAsnLeuThrAsnProLysSerIleValP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                                  TCGCTGGGGGCCATTCTCTTTACCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rValIle.....AlaPheGluValLeuLysTrpAlaG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCATGGTGTCGCGCAATAGTTTTCTTTATGGCCGCAAATCCGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                 TGCTGCGTCGCCAGCGCCTGTTCAATATCCTGATCGGGGTCGTGCTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                       lyProLysGlnMetLysAlaLeuAsnLysIlePheGlySerLeuPheMet 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTCGCATCCGTTTCGACCTTTTTGTCCAACCCGGCCATTCGAACCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpIleLysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTGATCAGTCTCTACACGCAATTCATCGGCAAGGACACGCCG...CTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnProGlnLeu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGATGACGGGTATTCTGACCAATGGTCTCAATCCGAAGACGTCGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGATGTCGAAGGCAGTCTGGTTCCCAGCGACAGATCGATGGGCCGGGA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCGGCCTATCTGGTCTATGCGGGCCTTGGCCACGGCCTTCAGCAAGATA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lyAlaAlaTyrLeuIleTrpLeuGlyIle...GlnGlnTrpArgAlaAla 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCATCCAGCATATTTTCCCCCAATATTCTGGATATCATCAAATTCGTCG
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                                                                                                                                                                                                   1668
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                                                                                                                                                                                                                                                                                                                                            202
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                                     HR; disease
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6
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               growth
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                   enhancer;
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stress resistance; transgenic plant; ds.

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC Sequences A61501-A61524 represent nucleotide sequences encoding CC Agrobacterium vitis hypersensitivity response (HR) elicitor proteins CC (B11630-B11688). The HR is a rapid, localised necrosis that is CC associated with the active defence of plants against many pathogens, and CC occurs when a pathogenic organism interacts with a nonhost plant (i.e. CC one in which intracellular bacterial growth and disease development do CC not occur). Like other HR elicitors, the A. vitis elicitor functions in CC in walling-off and killing of the pathogen. On grape plants, the A. vitis clicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor CC proteins, in non-infectious form, are used to treat plants or their seeds CC to impart resistance to disease, such as those caused by fungi, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide CC control insects, to impart resistance to environmental stresses, e.g., CC cold, and to improve nutritional value, e.g., altered oil content. The cs same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of CC control of previously untreatable diseases; provide systemic treatment; can and to improve nutrientable diseases; provide systemic treatment; can and to proteins or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment;
                                                                                                                                                                                                                                                             Align seg 1/1 to: A61502
                                                                                                                                                                                                                                                                                                          US-09-466-935-2 x A61502
                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
1070 CGGCCTCGATGGGCATTGCCATTGCCTGG......
                                                                                                                                                                            970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1668 BP; 342 A; 462 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and eliminate the need for biological control agents or polluting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium vitis
                                                                                                                                                                                                   10 LeuLeuThrSerIle.....IleLeuThrLeuSerProGlySerGlyAl
                                                                                                                                24
                                                                                      TGCCATGGTGTCGCGCAATAGTTTTCTTTATGGCCGCAAATCCGGGCTGG
                                                                                                                             alleAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGly.... 39
                                                                                                                                                                          CTGATTGCTTCGATAACCTGGCTGGCCGTTCTCAGCCCCGGCGCGCGATTT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           тJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-376567/32.
DB; B11635, B11636, B11637, B11638.
                                     ......GlyValTyrCysTrpAlaSerAspArgThrGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 86-87; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herlache TC, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107387.
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1.056
55.981
                                                                                                                                                                                                                                                             from: 1
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Percent Identity: 20.574
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                                                                                                                                                                                                                                                                                                                                                                                                                  209
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seq_documentation_block:
ID A48443 standard; DNA; 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1531 TCGCTGGGGGCCATTCTCTTTACCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1234 CGCGATGTCGAAGGCAGTCTGGTTCCCAGCGACAGATCGATGGGCCGGGA 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1134 GATCATCCAGCATATTTCCCCCAATATTCTGGATATCATCAAATTCGTCG
               Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 LeuValGlyAlaLeuLeuAlaSerAla 202
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                                             (AJIN ) AJINOMOTO KK.
                                                                                                              20-DEC-1999;
                                                                                                                                               28-JUN-2000.
                                                                                                                                                                              EP1013765-A1
                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                            L-threonine resistance; L-threonine synthesis; rhtC; L-homoserine; L-valine; L-leucine; ds.
                                                                                                                                                                                                                                                                                                                                                                             E. coli L-threonine resistance gene, rhtC
                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2000
                                                                                23-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 AspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCACCAATTGCTTTGGGGCCTGTTCATCTCCCTGTCGCATTTGCTGTG 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetGlnTyrIleValLeuGlyValThrThrIleValValAspIleIleVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnProGlnLeu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLe 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rValIle.....AlaPheGluValLeuLysTrpAlaG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTGCGTCGCCAGCGCCTGTTCAATATCCTGATCGGGGTCGTGCTCGCC 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTGATCAGTCTCTACACGCAATTCATCGGCAAGGACACGCCG...CTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyProLysGlnMetLysAlaLeuAsnLysIlePheGlySerLeuPheMet 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpIleLysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A48443
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
               Zakataeva NP,
                                                                                98RU-0123511
                                                                                                               99EP-0125406
                                                                                                                                                                                                                                             Location/Qualifiers 187..807
                                                                                                                                                                                                              /product= "RhtC"
               Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1557
                 Belareva AV,
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                 Tokhmakova IL;
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SXXCCCCCCCCCCXXX PFF XXXX

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alignment_block:
US-09-466-935-2 x A48443
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the L-threonine resistance gene, rhtC, from Escherichia coli. This sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-homoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-valine and L-leucine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 20
P-PSDB;
                                                                                                    575
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                                                                                                                                                                                                                                                                                                         475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 TGGGCATTACCTGCGGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 CTCTCAGACCGCTGTCAGTCGTTCCCGTAAAGAAGCGATGATGGGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 ATGGTGCACATTGTGGCGCTTATGAGCCCCGGTCCCGATTTCTTTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 840 BP; 165 A;
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ACCGCGCGCTGGGCATTTTTGCGCTGATCATTGTCGAAACGCTGGCGTG
                                                                                                                                                                                                                                                                                                         GAGGCGGTTTCTGCACCTGCGCCACAGGTCGAGCTGGCGAAAAGTGGGCG
                                                                                                                                                                                                                                                                                                                                                     LysSerLeuAlaSerThrGlnSerArgArgHisLeu......
                                                                                                                                                                                                                                                                                                                                                                                                             TCTGCTGGATGGGTTACCAGATGCTACGT.....GGTGCACTGAAAAAA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAATGGCCTGCCTACCCTGATTATGGTGGGCGGTGGCCTGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uValLeuLysTrp......AlaGlyAlaAlaTyrL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTTGGGCTGGGATTGCCCTGCCTTGGCCTGCATTTGATTATC.....GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyTrpArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...GlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAla 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rMetThrThrSerLeuAsnHisGlyTyrProAlaGly.....
                                               LeuMetGlnTyrIleValLeuGlyValThr......
                                                                                                                                                   alPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnProGln
                                                                                                                                                                                                     CAGTTTCCTGAAAGGTTTACTGACCAATCTCGCTAATCCGAAAGCGATTA
                                                                                                    TCTACTTTGGCTCGGTGTTCTCATTGTTGTCGGTGATAACGTTGGCACT
                                                                                                                                                                                                                                                 ....PheGlnArgAlaValPheValAsnLeuThrAsnProLysSerIleV 126
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DB; Y99598.
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1.119
49.772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.005
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seq_documentation_block:
ID A52691 standard: אמ
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                      The present sequence is the yggA gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        798
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                                                                                                                                                                                                                                                                                                                           30-DEC-1998;
09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A52691 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153
                                                                                                                                Disclosure; Page 24; 29pp; English.
                                                                                                                                                            protein
                                                                                                                                                                        Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid exci
                                                                                                                                                                                                                              WPI; 2000-414802/36
                                                                                                                                                                                                                                                          Tokhmakova
                                                                                                                                                                                                                                                                      Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1999;
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                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli; yggA gene; amino acid production; excretion protein gene;
ino acid excretion protein; ds.
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                                                                                                                                                                                                                  B01789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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99RU-0104431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                                                                                                      ΝP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                      Nakanishi K,
                                                                                                                                                                                                                                                                      Aleshin
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                                                                                                                                                                                                                                                                        Troshin PV;
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alignment\_scores

Sequence 636 BP;

120 A; 143 C; 180 G; 193 T; 0 other;

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seq_name:
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
LysG; LysE; ORF3; Lysine transport; regulatory protein;
                                DNA encoding LysG, LysE and ORF3 from Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                          158 eIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLeuTrpI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 nArgAlaValPheValAsnLeuThrAsnPro.....LysSerI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TGTGGTATGGTTTTGGCGCTTTTAAAACAGCAATGAGCAGTAATATTGAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 GTCGCCGTGGTTGCTGGCGCTGGTCACCTGGGGCCGCGTAGCCTTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 gSerValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GlyAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGlyTyrProAlaGly...GlyValTyrCysTrpAlaSerAspArgThr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 GCTCGGTCCACAAAATGCTTTTGTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 PheAlaTyr.........LeuLeuThrSerIleIleLeuTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValValAspi1 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...TTAGCCAGCGCCGAAGTCATGAAGCAAGGCAGATGGAAAATTATCGC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCAGTACCACATTATGATTGCCTTACTTTGTGCTATCAGCGATTTGGTC 147
                                                                                                                                                                                                                                                                                          TGCGCACGGCAAAAGCACAGCGCATTATCAATCTGGTTGTGGGATGTGTT 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACCATGTTGGCAGTGACCTGGCTGAATCCGCATGTTTACCTGGATACTT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLys 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTCTTATTACTTTCAAGGTCTTGCACTTGGGGGGGGCTATGATCCTACC
                                                                                                                                                                                                                         ATGTGGTTTATTGCCTTGCAGCTGGCG
                                                                                                                                                                                                                                                          PheMetLeuValGlyAlaLeuLeuAla
                                                                                                                                                                                                                                                                                                                       leLysGlyProLysGlnMetLysAlaLeuAsnLysIlePheGlySerLeu 191
                                                                                                                                                                                                                                                                                                                                                           AAA.....CGCTGGTTTGCACTCGGG.....ACAATTAGCGCCTCTTT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGTTGTACTGGGCAGCCTTGGCGGCCAA.....CTTGATGTGGAACCA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnPro 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....CTGATTTGCGCCGGGATTTTTGGTGGCAGCGCGTTATTGATGCA 191
                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:T96816
                                                                  (first entry)
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0.926
58.373
                                                                                                                                       DNA; 2374
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Gaps:
Percent Identity:
                                                                                                                                       ВP
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10
24.880
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                                                                                                                                                                                                                                                                                                                                                           520
 export protein;
                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                       Align seg 1/1 to: T96816
                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                      US-09-466-935-2 x T96816
                                                  1075 CATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGCGAAG
                                                                                                                     1025 ATGGAAATCTTCATTACAGGTCTGCTTTTGGGGGGCCAGTCTTTTACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                        LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.

NB. This sequence has been created from the information given in table 2
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2374 BP;
                                                                                                                                                                                                                                                                                                                                                                                                          of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23 and 26; Page -; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-333867/31.
P-PSDB; W37714-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eggeling L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KERJ ) FORSCHUNGSZENTRUM JUELICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE19548222-A1
   35 lyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyAsp 51
                                                                                    19
                                                                                                                                                   3 LeuGluTrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLeuSe
                                                                                  rProGlySerGlyAlaIleAsnThrMetThrThrSerLeu...AsnHisG
                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated from Corynebacterium glutamicum, contains the LysG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sahm H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95DE-1048222
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1.078
47.429
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= LysE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1016..1726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                          526 A;
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                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                          640 C;
                                                                                                                                                                                                                                                                        Percent Identity:
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                                                                                                                                                                                       to:
                                                                                                                                                                                                                                                                                                                                                                           648
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560 T; 0 other;

20.571

1124

1074 35

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seq_documentation_block:
ID V27579 standard; DNA; 2289 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1423 CGATAAGCAGCGGGTTTGGGTAAAG 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294
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This nucleotide sequence encodes human hepatocyte nuclear factor 4 isoform alpha 4 (HNF4 alpha 4). Sequences are also provided for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1219 GATCGTGCTCGATATTATGCGCTGGGGTGGCATCGCTTACCTGTTATGGT
                                                                                      Claim 11; Fig 3; 43pp; English.
                                                                                                                                                   Use of hepatocyte nuclear factor 4 - for developing products for diagnosing and determining risk of diabetes and for identifying agents for treatment of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatocyte nuclear factor 4; HNF4 alpha 4; human;
non-insulin-dependent diabetes mellitus; NIDDM; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 heIleMetProGlnGlnProGlnLeuMetGlnTyrIleValLeuGlyVal 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 nLeuThrAsnProLysSerIleValPheLeuAlaAlaLeuPheProGlnP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 AlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPheValAs 118
                                                                                                                                                                                                                                                                          WPI; 1998-322753/28
                                                                                                                                                                                                                                                                                                                                        Krolewski AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9823780-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human hepatocyte nuclear factor 4 isoform alpha 4 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V27579;
                                                                                                                                                                                                                                                                                                                                                                                              (JOSL-) JOSLIN DIABETES CENT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 aGlnArgIleAlaLeuTrpIleLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrThrIleValValAspIleIleValMetIleGlyTyrAlaThrLeuAl 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATTGAAGAAACAGAACCAACCGTGCCCGATGACACGCCTTTGGGCGGT 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCATTGCGGTTCTTCTCGTGTGTTTAATTTCTGACGTCTTT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSerVa
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1141 CTGCACCTGGGAACGCAGCCGCTTGATCTTCCCTGGATCGCTCAGCCCCT 1092

160 ValMetIleGlyTyrAlaThrLeu......AlaGlnArgIl 171

CGGCCACGCGAGTCATACTGGCGGTCGTTGATGTAGTCCTCCAAGCTCAC

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alignment_block:
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                                                                                                                                                                                                                                                             1335
                                                    1241 GCCACGTGATGCTCTGCAAGGTGGGCAGCAGCAGCAGCAGCTCTCCAAAG 1192
                                                                                                                                                                                                                                                                                                                                                                  1385 TATGTTCCTGCATCAGGTGAGGGTGCAGGGGGTGGTGGGCATGGGGTGCA 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1471 CTGTCCCCTGGGTCGGGGCCACTCACATCTGTCCGTTGCTGAGGTGAG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1421 TGGG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes, especially non-insulin-dependent diabetes (NIDDM). Also claimed are: (1) a method for evaluating an agent for use in treating diabetes by evaluating the effect of the agent on an aspect of HNF4 metabolism; (2) the agent identified in (1); (3) a method for treating a cell having an abhormality in structure or metabolism of HNF4, comprising administering the agent to the cell; (4) a method for producing a fragment or analogue of HNF4 polypeptide having wild-type activity; and (5) a method for producing an HNF4 polypeptide or fragment or analogue having a non-wild type activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoforms alpha 1 (see V27577), alpha 2 (see V27578) and gamma (see V27580). HNF4 is a transcription factor whose ligand has not yet been identified. The isoforms of HNF4 are reported to be derived from alternative splicing events. The alpha isoforms have been mapped to chromosome 20 and the gamma isoform to chromosome 8. A claimed method for determining if an animal is at tisk of developing diabetes, comprises evaluating an aspect of HNF4 metabolism or structure in the animal. especially as related to HNF4 from chromosome 20. An abnormality in the aspect of HNF4 metabolism or structure is diagnostic of being at risk for
                                                                                                                                                                                                                                                                                               101 euAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPheVal 117
                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2289 BP; 489 A; 723 C; 653 G; 424 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 spSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSer 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 sGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 LeuSerProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHi
                                                                                                                                                         AATCITGGCCATGCCGAAGAGCTTGATGAACTGGATCTGCTCGATCATCT 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTr
.....TyrIleValLeuGlyValThrThrIleValValAspIleIle
                                                                                                    eProGlnPheIleMet.....ProGlnGlnProGlnLeuMetGln. 145
                                                                                                                                                                                                      AsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeu.....Ph 132
                                                                                                                                                                                                                                                           TCGCTGGGGGACCCTCCCAGCAGCATCTCCTGCAACAGGTT.....GTC
                                                                                                                                                                                                                                                                                                                                                                                                                    pLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSerL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....CATTGTGTTGGCAACGATGACGTTGGTTCC........
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171 eAlaLeuTrpIleLys 176 :::::::|||:::|||

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seq_documentation_block:
ID X13048 standard; DNA;
AC X13048;
AC X14-NOV-1999;
AC X12-NOV-1998;
AC X14-NOV-1997;
AC ACMAY-1997;
AC A COMPUTER TREADABLE |
AC X12-NOV-1997;
AC X13-NOV-1997;
AC X14-NOV-1997;
AC X15-NOV-1997;
AC A COMPUTER TREADABLE |
AC X12-NOV-1999-045171/04.
AC COMPUTER TREADABLE |
AC A COMPUTER TREADABLE |
AC COMPUTER TREADABLE |
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                                                                                                                                  alignment_block:
US-09-466-935-2 x X13048/rev
                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                 Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 700-703; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-045171/04.
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7 PheAlaTyrLeuLeu......ThrSerIleIleLeuTh 17
                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                              Ratio:
                                                                 to reverse of: X13048
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97US-0044031.
97US-0046655.
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0.859
41.597
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Gaps:
                                                                    to: 6590
                                                                                                                                                                                                                                          238
9
18.908
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5143	TTTGCTTATTTAGCTCTTTACACTGGGATTAACAGTGCCAGCGTTTTTGG 5	5094
17 5093	rLeuSerProGlySerGlyAlaIleAsnThrMetThrThrS 3 :::   :::     ::::: rGCAACGCCAGCGTTGGGTGGTGTTATTGGGGCAGTCACAATGTTAACAG 5	31 5044
31	Asp	47
5043	GAATGAATCCGGATGCTCCAATCAGTAATATTTTC	5009
4 8		64
5008		4973
64	AlaT	81
4972	ATCGGTGTTATTT 4	4960
81	eTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAsp	97
4959	TTGCCGTATGG4	4949
98		114
4948		4899
114		130
4898	_	4849
130	aLeuPheProGlnPheIleMetPro	138
4848	CTATTTTCTTAATCATGCCTGTAGCCGGAGCTATTTCTAATGGC 4	4805
139		146
4804	TTAGTTGGTATTATCAATGTTGTCTTAGAAAAAGGTGGCATGGTTGCTGG 4	4755
146		152
4754	CTTTACTCTTGGTTTAACCTTSTTGCCAATGGTAATGTTTGGTTTACATC	4705
153		153
4704	-	4655
154		170
4654	TTGTTATTACCAATTCTGGCCATGGCTGGTGCGGGACAAGTCGGTGCAGC	4605
170		187
4604	TTTAGCATTATGGATTCGTTGTAAATCAGATAAAAAATTAGTTGAAATGA	4555
187	lePheGlySerLeu 191	
4554	TTAAAGGTGCCTTG 4541	

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Database: Issued_Patents_NA:*
Database sequences: 302521
Database length: 87301344
Search time (sec): 80.320000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             About: Results were produced by the GenCore software, version 4.5. Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/ina/backfiles1.seq:5474933-3 + 188.00 388.64
/cgn2_6/ptodata/2/ina/backfiles1.seq:US-08-476-254-6 + 184.00 379
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-927-219-78 - 82.50 14%
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-976-074-4 + 79.50 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-976-074-4 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score_list:
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-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
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-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER_US9466935_@CGN1_1_59 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of: US-09-466-935-2 to: Issued_Patents_NA:*
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142.45 2.39
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;Patent No. 5474933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
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                          474
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Ratio:
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-558-107-1 - /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-243-539-1 - /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-390-878-17 - /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-276-531-19 + /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-276-531-21 + /cgn2_6/ptodata/2/ina/6B_COMB.seq:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-466-935-2 x 5474933-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: EINER, RONALD M.; FUQUA JR., TITLE OF INVENTION: MARINE MELA GENE NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 AATGGGTCGGTGGGCTCTATCTTGGTTACATCGGCATTAGCATGTGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 ATGGTTGGTGAGCTAGCAGGCGTTGCCCTCGTGGCGATTGCCGCCGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 ACTGGCCATGACTCTCGGTATGAGTATCGGTGTG.........
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FILING DATE: 10-NOV-1992
APPLICATION NUMBER: 496,804
FILING DATE: 21-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaAlaGlyAlaIle...AspLeuLysSerLeuAlaSerThrGlnSerAr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValValAs 157
                                                                                                                                                                                                                                                                                         gArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS 124
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                                                                                 GCTGGGCCTTTATGATGTCGCTGCTCCCCCCTTTTATCAGCGTTGACCAA
                                                                                                                                                                                                                                             TCGAGCGCTAATAACTCAAGGCTTTGTCACCGCCAATGCTAATCCAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                        GCCAAAGGGAAAATGGCCAACCTTGACAATACCTCCAGTCAGATCAGTAA
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                                                                                                                                                           \verb|erIleValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln|
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Percent Identity:
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56.30
60.96
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Sequence 6, Application US/08476254
Patent NO. 5846531
GENERAL INFORMATION:
APPLICANT: WEIMER, RONALD M.
APPLICANT: FUQUA, WILLIAM C.
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: WATSON COLE STEVENS DAVIS, P.L.L.C.
STREET: 1400 K STREET NW
                                                           alignment_block:
                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                            ; LOCATION:
US-08-476-254-6
                                                                                          Quality:
Ratio:
Percent Similarity:
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 Align seg 1/1
                                       US-09-466-935-2 x US-08-476-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,254
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, JAMES A.
REGISTRATION NUMBER: 31,714
REFERENCE/DOCKET NUMBER: JAP30319C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-0088
TELEPHONE: 202 628-0088
TELEPHONE: 202 628-008
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202 628-8034
                                                                                                                                                                                                                                                                   ANTI-SENSE:
FEATURE:
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HYPOTHETICAL:
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Percent Identity: 27.619
from: 1
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 to: 720
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HNF-1BETA

	STREET: P.O. Box	
	CORRESPONDENC ADDRESSEE:	
BILITY NF) 1 ALPHA	TION:	
	APPLICANT: Horikawa, Yukio APPLICANT: Menzel, Stephen	
	APPLICANT: Kaisak: APPLICANT: Furuta	
	APPLICANT: Yamagata, Kaz APPLICANT: Oda, Naohisha	
	GENERAL INFORMATION: APPLICANT: Bell, Graeme	
	s eq	
	<pre>seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-927-219-78</pre>	
	191 LeuPheMetLeuValGlyAlaLeuLeuAla 200	
190 672	4 rplleLysGlyProLysGlnMetLysAlaLeuAsnLysIlePheGlySer ::::::: ::::::   :::   :::	
622	GTTCTTCAGCATGCTTATGCGAGCGG.CGGAAAACCCTTAAACTGT	
573		
157	<pre>1 ProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValValAs    </pre>	
523	:: ::   ::: :::	
140		
124 473	107 gArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLysS: :	
423		
107		
91 373	75 ysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArg	
323	GGGTGTCGCCAGTATGATGCTGAACTATCCACAACTCTTCGATATTTTAA	
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273	A TGGTTGGTGAGCTAGCAGGCGTTGCCCTCGTGGCGATTGCCGCGTAAT	
3 6 5	SO GIVENICIONE POSCONE CONTROL	
ာ ထ	rCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaGlyTrpArg	
205	23 EASTITIMETITITISETLEUASTHISGIYTYPTOALAGIYGIYVAIT :::       172 ACTGGCCATGACTCTCGGTATGAGTATCGGTGTG	
171	2 ITTTTACCGACCTTTTTTTCGTCTCAATTACACCAGGTATGTGTATGAC	
25	9 TyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaII 1 ::::::::::::::       2 :::	

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alignment_block:
US-09-466-935-2 x US-08-927-219-78/rev
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; LOCATION:
US-08-927-219-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: US-08-927-219-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                     1186
                                                                                                                                                                                                                               1216
 1134
                                                                          1184 TATGTTCCTGCATCAGGTGAGGGTGCAGGGGGTGGTGGGGGTGCA 1135
                                                                                                                                                                                                                                                                                                        1220 TGGG.....
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FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/029,679
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APPLICATION NUMBER: US/08/927,219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1441 base pair
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                                     101
                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                51 spSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerArgSer 67
                                                                                                                                                                                                                                                                                                                                           34 sGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyA 51
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                     ValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTr 84
TCGCTGGGGGACCCTCCCAGCAGCATCTCCTGCAACAGGTT.....GTC 1091
                                 euAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPheVal 117
                                                                                                      pLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLysSerL 101
                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
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20..1414
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1.019
47.093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARCD: 272
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                                                                                                                                                                                                                                                                                                  ..... 1217
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                                                                                                                                                  .....CA 1185
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-976-074-4
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                                                          alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08976074 Patent No. 5840847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                             TELEFAX: (732) 594-4720 INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1040 GCCAGGTGATGCTCTGCAAGGTGGGCAGCAGCAGCAGCAGCTCTCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1090 AATCTTGGCCATGCCGAAGAGCTTGATGAACTGGATCTGCTCGATCATCT 104:
                                                                                                                                        STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,074
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                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RUSHMORE, THOMAS H.
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA Encoding Prostaglandin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               890 TGGCATCTGGGTCAAA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 eAlaLeuTrpIleLys 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               940 CTGCACCTGGGAACGCAGCCGCTTGATCTTCCCTGGATCGCTCAGCCCCT 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 ValMetIleGlyTyrAlaThrLeu.....AlaGlnArgIl 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990 CGGCCACGCGAGTCATACTGGCGGTCGTTGATGTAGTCCTCCAAGCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 eProGlnPheIleMet......ProGlnGlnProGlnLeuMetGln. 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 AsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeu.....Ph 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....TyrIleValLeuGlyValThrThrIleValValAspIleIle 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: J. Mark Har
P.O. Box 2000
                                                                                                                                                                                                                                                                                  (732)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRYGORCZYK, RICHARD
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79.50
0.710
53.081
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Box 2000 - 126 E. Lincoln
    Percent Identity:
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                  Length:
Gaps:
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Avenue
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22.275
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seq_documentation_block:
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US-09-466-935-2 x US-08-976-074-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-976-074-4 from: 1 to:
                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08083741 Patent No. 5869281
                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
APPLICANT: GRYGORCZYK, RICHAF
APPLICANT: METTERS, KATHLEEN
APPLICANT: NGUYEN, TRUYEN
                          CORRESPONDENCE ADDRESS:
                                               APPLICANT: RUSHMORE, THOMAS H.
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA Encoding
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 tLeuValGlyAlaLeuLeuAlaSerAlaArg 203 :|||:::||| |||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521 ATAAAGAA.....TGGATCCGCTTT...GACCAATCAAATGTC 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 TCCAAGGCATCGTTTCTGCTTTTGGCCAGCGGCCTGGTAATCACTGATTT 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 TCGCCATTCTCATGAAGGCATATCAGAGATTT.....AGACAGAAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 CCACAACAATGTCCATGAACAATTCCAAACAGCTAGTGTCTCCTGCAGCT 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 eAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTGCAGTATTTTTGGTATCTGCATGGTGTTTTCTGGTCTGTGCCCACT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euAlaGlnArgIleAlaLeuTrpIleLysGlyProLysGlnMetLysAla 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTCTAGGCAGTGTGATGGCCATTGAGCGG 636
W. Wallen,
                                                                                                                                                                                                                            RICHARD
                                                                               Prostaglandin
                                                                               Receptor FP
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alignment_block:
US-09-466-935-2 x US-08-083-741-4
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;; TYPE: nucleic acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-083-741-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-083-741-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (908)594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/083,741
FILING DATE: 25-UN-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W.
REGISTRATION NUMBER: 35,403
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                195 GAGAGGGAGATGACTTGAGTGG......TTGGCTTTTATCT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                 145 CTGGCGGCCTGGGATGACAAGATGTCTGGACTGCAATCCTGCACAGTTTT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 GAGCGGCTCCTTCTGC.....TCCTCAGAGAGCCCGG
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: F.
TITY: Rahway
TITY: Town Je
                                                                                                                                                                                                                                                                                                                                                                                  69 eAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 ysAlaGly.TrpArgGly...valGlyThrLeuPheSerArgSerValI1 69
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ZIP: 070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                            AlaIleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLeuPh 111
TCGCCATTCTCATGAAGGCATATCAGAGATTT.....AGACAGAAG 420
                                        leValPheLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnPro 141
                                                                                  TTTTTCAGTAATCTTCATGACAGTGGGAATCTTGTCAAACAGCCTTGCCA
                                                                                                                    eGlnArgAlaValPheValAsn.....LeuThrAsnProLysSerI 125
                                                                                                                                                                        GCGCTTCTTTCAAACACAACCTGCCAGACGGAAAACCGGCTTTCCGTATT
                                                                                                                                                                                                                                                        CCACAACAATGTCCATGAACAATTCCAAACAGCTAGTGTCTCCTGCAGCT
                                                                                                                                                                                                                                                                                               lyIle......GlnGlnTrpArgAlaAlaGly 94
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Percent Identity: 22.275
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                                                                                     379
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-764-233A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,233A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 1506/CIP6
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8589
TELEPAX: (919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                     TELEFAX: (919) 541-861 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 TCCAAGGCATCGTTTCTGCTTTTGGCCAGCGGCCTGGTAATCACTGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556 CTTTGCAGTATTTTTGGTATCTGCATGGTGTTTTCTGGTCTGTGCCCACT 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Neff, Snezanna
APPLICANT: Ryals, John A.
TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 tLeuValGlyAlaLeuLeuAlaSerAlaArg
                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 49377 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                 ORIGINAL SOURCE:
                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                           TOPOLOGY:
                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euAlaGlnArgIleAlaLeuTrpIleLysGlyProLysGlnMetLysAla 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.....leValMetIleGlyTyrAlaThrL 167
                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValValAspIl 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCTAGGCAGTGTGATGGCCATTGAGCGG
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Beck, James J.
Hill, Dwight S.
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                                                                           linear
               Sorangium cellulosum
                                                   DNA (genomic)
                                                                                         single
                                                                                                                                                                                                                                                 1506/CIP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version
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OTHER INFORMATION:
alignment_block:
US-09-466-935-2 x US-08-764-233A-1
                                                                                                    alignment_scores:
                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 383..760 OTHER INFORMATION: /proc OTHER INFORMATION: /note OTHER INFORMATION: the r OTHER INFORMATION: Sacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: 927..19874
OTHER INFORMATION: /proc
OTHER INFORMATION: /nott
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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LOCATION: 13455..19616
OTHER INFORMATION: /product= "Module 3 of Sora"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 35528..40114 OTHER INFORMATION: /pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 30881..35446 OTHER INFORMATION: /pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /product= "SorB" OTHER INFORMATION: /note= "Gene pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 7203..12884
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                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 46851..47891
                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                              LOCATION:
                                                                                      Quality:
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                                                                     Ratio:
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19870..24556
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19871..46318
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40190..46318
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24638..30820
                                                     79.50
1.445
53.398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "SorA"
/note= "Gene product is highly homologous to type I PKSs are known to be involved in the synthesis of polyketide compounds."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This gene encodes a protein that is highly homolog the reductase domains of type I PKSs such as eryA from Saccharopolyspora erythraea."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Module 1 of
                                                                                                                                                                        /product= "SorM"

note= "The protein encoded by the sorM gene is highly homologous to the methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "SorR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product=
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                                                                                                                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                                                   /product= "Module 5 of SorB"
                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Gene product is highly homologous to type I PKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Module 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Module 1 of SorB"
                                                                                                                                                                                                                                                                                                                                                                                           "Module 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Module
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                                                          32.039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SorB"
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Align seg 1/1

to: US-08-764-233A-1

from: 1

to: 49377

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1492
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                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1281 GCCTGCCGGTTCCCGGGGGCGCCGGACGTGGACAGCT.....ACTGGAG 1324
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 09
FILING DATE: 01-SEP-1993
                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VRANG, ASTRICTIFILE OF INVENTION: ReconTITLE OF INVENTION: ContaTITLE OF INVENTION: Same
ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1579/92
FILING DATE: 30-DEC-1992
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                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 07-JAN-1994 CLASSIFICATION: 435
                                         FILING DATE:
                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eGlnArg 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrLeuPheSerArgSerValIleAlaPheGluValLeuLysTrpAlaG1 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTCCTATCCGGCGGCGTGGATGCGGTCACCGAGGTGCCCGCTGGCCGGT 1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Foley & Lardner
F: 3000 K Street, N.W.
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOHANSEN, Eric
NILSSON, Dan
VRANG, Astrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISRAELSEN, Hans
BECH HANSEN, Egon
                                                                                                  03-JAN-1994
                                         25-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Lactic Acid Bacterium Containing an Inserted Promoter and
                                                                                                                        PCT/DK94/00004
                                                           US 08/036,681
                                                                                                                                                                                   DK 0988/93
                                                                                                                                                                                                                                                                                                                               US/08/179,557
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US-08-179-557-16
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    Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30307/140/PLVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                     571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 TGGCGGGCAGGGATTTTGCTTTCAATCTTGGTAACAACTATCTTGGCTCT
                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 CATTGACTTCAATCTTTGACCCAATCGGAACTTTCATCGGAACTGGTCGC 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 TTTGACTGGCGTGGTTAAAGTTGATGTGAATACTTTATTTGCTGAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 yrLeu.....IleTrpLeuGlyIleGlnGlnTrpArg 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GlyAspSerTyrCysAla.....GlyTrpArgGlyValGlyThrLeuPh 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 snHisGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGTTCCAACACAAGCAACAGCACCAATTTTGATTATCGTTGGGATGATG 770
                                                                                    AACAGCAATTATGTTTGCTATCTCAAGCTTGTTCTTACCACTTCTTGCGA
                                                                                                                                                                                                                                                                                                          snProLysSerIleValPhe.....
                                                                                                                                                                                                                                                                                                                                                                               nSerArgArgHisLeuPheGlnArgAlaValPheValAsn...LeuThrA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGACAGGAATCTTTACTGATGAAGATTTGAAAGACATGGAAACCAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAlaGlyAlaIle......AspLeuLysSerLeuAlaSerThrGl 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eSerArgSerValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAACAACCTTTGGTGCAGCATTTGGTCCAAAAGGATTTGGTTCTTTATT
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                                       euGlyValThrThrIleValValAspIleIleValMetIleGlyTyrAla
                                                                                                                               eProGlnPheIleMetProGlnGlnProGlnLeuMetGlnTyrIleValL 149
                                                                                                                                                                              TCTGCTGCCGGAATCGGTGCAGGAGGACGTACTGGTCTTGCATCAGTTGT 670
                                                                                                                                                                                                                                                                CTCCAATCGGAGCAATTTTCGGAACATCAAATACAACCGTTTATGTTGAG
                                                                                                                                                                                                                                                                                                                                                         TGGTTTCTCATCAAAAATGGACAAAGCTTTGTTTGCTGACATGATTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTGATTCATCACGTTATATTGAAGTATTAATGACAGTTCTTGCTTTCT
                                                                                                                                                                                                                 .....LeuAlaAlaLeuPh 132
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49.561
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Percent Identity: 22.807
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Align seg 1/1 to: US-08-927-219-130

from: 1

to: 10014

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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-927-219-130
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alignment_block:
US-09-466-935-2 x US-08-927-219-130
                                                                                                                                                             US-08-927-219-130
                                                                                                       alignment_scores:
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                                                   Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-007-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 sAlaLeuAsnLysIlePheGlySerLeuPheMet 193
                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: AR TELECOMMUNICATION INFORMATION: TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60 FILING DATE: 02-OCT-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                              LENGTH:
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                                                                                     Quality:
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                                                                                                                                                                                                             nucleic acid
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Furuta, Hiroto
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                                                                                                                                                                                                                                                                                     512/474-7577
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                                                                                                                                                                              linear
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                                                  78.00
0.867
46.392
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147
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                                                                                                                                                                                                                                                                                                                                                        37,259
                                                     Percent
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                                                   Gaps:
: Identity:
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22.680
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-27
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/08444644 Patent No. 6015555
                                                                                                                                                                                                                                                                       GENERAL INFORMATION: Phillip M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERR
TITLE OF INVENTION: CONJUGATE
TITLE OF INVENTION: CONJUGATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5669 GTTTCTTGCCCAAGGACAC.....AGCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 GlyValThr.....ThrIleValValAspIleIleValMetIleGlyTy 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 euMetGln.....TyrTleValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 eLeuAlaAlaLeuPheProGlnPheIleMetProGlnGln...ProGlnL
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 lyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisLeu 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 spargThrGlyAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeu 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 IleIleLeuThrLeuSerProGlySerGlyAlaIleAsnThrMetThrTh 30
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                           STATE: P
                                                                                                                                                                                 STREET:
                                                                                                                                                                                                         ADDRESSEE:
  OPERATING SYSTEM:
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                                                                                           02173
                                                                                                                                                           Lexington
                                                                                                                                      MA
                                                                                                                                                                                      Two Militia Drive
                                                                                                                USA
                                                                                                                                                                                                         Hamilton,
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 TRANSFERRIN RECEPTOR SPECIFIC ARBITOMETRIC AGENT ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                                                                                                                                            CONJUGATES
                                                                                                                                                                                                                                                      46
                                                                                                                                                                                                      Brook, Smith & Reynolds, P.C
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alignment_block:
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                                                       6445
                                                                                                                   6410 AAG...GTTTCAATATTCTTTACTGCCACCGCCATCGCC.....
                                                                                                                                                                                                                                                             6310 AATATACAACCCAACTGAAGCTACCGGACGCGTGACCTGCTGGCAACGCA 6359
                                                                                                                                                                                                                                                                                                                                  NAME: Wagner Richard W.
REGISTRATION NUMBER: 34.480
REFERENCE/DOCACT NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPANE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                            6360 CGCCTGGCTGCGTTTCTACATCTACCGGCGGCAGTTTTTGCGCAGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 10785 base pairs
TYPE: nucleic acid
           91 rgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArg 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
                                                                                74 uLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpA 91
                                                                                                                                                              58
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MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     32 ....LeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrp......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..10785
OTHER INFORMATION: /note=
OTHER INFORMATION: Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: PAH4625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 07-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                .....AlaSerAspArgThrGlyAspSerTyrCysAlaGlyTrp 57
                                                                                                                                                       ArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGluValLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                6445
                                                                                                                                                                                                                                                                                                                                                                                                             to: US-08-444-644-27
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47.337
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Percent Identity: 25.444
"Function = "Expression
Coding Sequence""
                                                                                                                                                                                                                                                                                                                                                                                                             from:
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seq_documentation_block:
; Sequence 41, Application US/08444644
; Patent No. 6015555
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                                                                            TELEFAX: (617) 861-95
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                           NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6569
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 10844 base pai
                                                                                                                                                                                                               APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6646 CTGG 6649
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                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US90/05077 FILING DATE: 07-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 26-NOV-
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APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uTrp 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTTTATCAAACTTCGCGCTGTATTCCCGCAGGGCCTCATCGCCGCGT. 6568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerIleValPheLeuAlaAlaLeuPheProGlnPheIleMet.ProGlnG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGACACCTT..
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                nucleic acid
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                                                                                             861-9540
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                                                                                                                                                                                                                                                                                                                                                                             US 07/800,458
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                                                                            41:
                                                                                                                                                        ALK88-15AAAZ
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25
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alignment_block:
US-09-466-935-2 x US-08-444-644-41
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                                                                       seq_documentation_block:
                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-444-644-18
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                      Sequence 18, Application US/08444644 Patent No. 6015555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8612
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                                                                                                                                                                                                                    173
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                    uTrp 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCTGGCTGCGTTTCTACATCTACCGGCGGCAGTTTTTTGCGCAGTGTGG
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                                                                                                                                                                                                                                                                   ACAGTGCGGGTAATGCTTTCAGAGGCGGAAATCGCCGGGCGCGTTAACAG 8763
                                                                                                                                                                                                                                                                                                           AspIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLe 173
                                                                                                                                                                                                                                                                                                                                                                                                       lnProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValVal 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerIleValPheLeuAlaAlaLeuPheProGlnPheIleMet.ProGlnG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArg 107
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Vector Coding Sequence""
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alignment_scores:
Quality:
                                                                                                                         alignment_block:
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                                                                  Align seg 1/1
                                                                                                        US-09-466-935-2 x US-08-444-644-18
                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Friden, I
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: do
TOPOLOGY: circul
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/232,246
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                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: pAH4602
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                             21 GlySerGlyAlaIleAsnThrMetThrThrSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US90/05077 FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1..11528
OTHER INFORMATION: /note= "Function="Expression Vector
OTHER INFORMATION: Coding Sequence""
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REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Two Militia Drive
                                                                     to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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VENTION: TRANSFERRIN RECEPTOR SPECIFIC
VENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                                                                                                                                                                                                                                                                          NO
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                                                                     US-08-444-644-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                          77.50
0.969
47.337
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                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith & Reynolds, P.C
                                                                       from: 1
                                                                                                                                                                                              Length:
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                                                                                                                                                             25.444
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seq_documentation_block:
; Sequence 32, Application US/08444644
; Patent No. 6015555
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9400 ACAGTGCGGGTAATGCTTTCAGAGGCGGAAATCGCCGGGCGCGTTAACAG 9449
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                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/444,644
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9450 CTGG 9453
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                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION UNMBER: US 07/800,458
FILING DATE: 26-NOV-1991
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ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 lnProGlnLeuMetGlnTyrTleValLeuGlyValThrThrIleValVal 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9214 AAG...GTTTCAATATTCTTTACTGCCACCGCCATCGCC......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 uTrp 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AspIleIleValMetIleGlyTyrAlaThrLeuAlaGlnArgIleAlaLe 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 uLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
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                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..ArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLys 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..TGTTTTAGCTCGTCGCTCAGGCGTTCGCTGGCGGCGGCGATCTCCTCT 9297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArg 107 ::: :::::: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGluValLe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....LeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrp......
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                                                                                                                                                                                                                                                                                                                                                                                                USA
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1 156	140 lnProGlnLeuMetGlnTyrIleValLeuGlyValThrThrIleValVa
G 140 . 7910	124 SerIleValPheLeuAlaAlaLeuPheProGlnPheIleMet.ProGlnCienter
s 123 : 7861	108ArgHisLeuPheGlnArgAlaValPheValAsnLeuThrAsnProLy:
g 107 T 7835	91 rgAlaAlaGlyAlaIleAspLeuLysSerLeuAlaSerThrGlnSerArvii: ::::::
. 7787	7787
A 91	74 uLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnTrpA
.e 74 . 7787	58 ArgGlyValGlyThrLeuPheSerArgSerValIleAlaPheGluValLe :::         :::         :::   ::::
p 57     7751	rGlyAspSerTyrCysAlaGlyTr         :::          :::
. 44 A 7701	32LeuAsnHisGlyTyrProAlaGlyGlyValTyrCysTrp
. 31 G 7651	21 GlySerGlyAlaIleAsnThrMetThrThrSer
	Align seg 1/1 to: US-08-444-644-32 from: 1 to: 12127
	alignment_block: US-09-466-935-2 x US-08-444-644-32
	alignment_scores: 77.50 Length: 169 Quality: 77.50 Gaps: 9 Percent Similarity: 47.337 Percent Identity: 25.444
	IMMEDI CLON FEATUR
	MOLECU
	STRA
	SEQUEN LENG
	INFORMAT
	TELECOMMUNICATION INFORMATIC TELEPHONE: (617) 861-6240
	REGISTRATION REFERENCE/DO
	ATTORNEY/AGENT
	APP) FIL
	FILING DATE: 07-SEP-1990  PRIOR APPLICATION DATA:
	PRIOR APPLICATION DATA:

Quality:

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seq_documentation_block:
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LOCATION: US-08-927-219-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46,
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                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7988 CTGG 7991
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewitl
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION: AND HNF-4ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                    FEATURE:
                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 61 FILING DATE: 02-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                    LENGTH: 844 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                     NAME/KEY:
                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                               Wilson, Mark B.
Wilson, Mark B.
77,259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaisaki,
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                                                                                                                                                                                   512/474-7577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horikawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0,
                  429..515
                                                                       linear
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                                                                                                                                                                                                                                                                                                                               us 60/025,719
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alignment\_scores

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alignment_block:
US-09-466-935-2 x US-08-927-219-46
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Percent Similarity:
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 1125
                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08878801 Patent No. 6004808
                                                                     APPLICANT: Negulescu, Paul
APPLICANT: Negulescu, Paul
APPLICANT: Offermanns, Stefan
APPLICANT: Offermanns, Stefan
APPLICANT: Zuker, Charles
FITTLE OF INVENTION: PROMISCUOUS G-PROTEINS COMPOSITIONS AND THEIR USE
FILE REFERICE: 08366/02001
CURRENT APPLICATION NUMBER: US/08/878,801
CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: US 60/020,234
EARLIER FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 ATGTTGCTTACAGTTTCATCAGGCACACAGAAGAGGCCCCAGCACGAAGCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 GTGCTGCTCCTAGGTGAGGCGGCTGCCTGCCCTGGCCAGGGCTCCAGGGA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 GCGAGCACCTGCTCGGAGCCACCAAGAGATCCATGGTGTTCAAGGAC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 etGlnTyrIleValLeuGlyValThr.....ThrIleValValAspIle 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 eLeuAlaAlaLeuPheProGlnPheIleMetProGlnGlnProGlnLeuM 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 GGAGCATTAAGCTGACTTGCCCAGCGTCACTGAGTTGGCTACGGGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 TTTTATG.....ATGCCCATTTCACAGTTCAGGCAGGTAGAGGCAGAGG
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65 erArgSerValIleAlaPheGluVal 73	Align seg 1/1 to: US-08-453-695A-113 from: 1 to: 2347	alignment_block: US-09-466-935-2 x US-08-453-695A-113	alignment_scores: 75.50 Length: 76 Quality: 75.50 Gaps: 4 Percent Similarity: 61.842 Percent Identity: 32.895	SEQUENCE SERGTH TYPE: STRAND TOPOLO MOLECULE MOL453-695	INFORMATION	TELEPHONE: 312/474-6300 TELEFAX: 312/474-0448	REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 326	CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: No. 5708143and, Greta	APPLICATION NUMBER	OPERATING SYSTEM: PC-DC SOFTWARE: Patentin Rele	MEDIUM TYPE: Floppy dis COMPUTER: IBM PC compat	ZIP: 60606 COMPUTER READABLE	CITY: STATE: COUNTRY	STREET: 233	ADDRESSEE: Marshall	NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS:	APPLICANT: Suzuki, Shintaro	INFORMATION	INNERNATION: COANT: Suzuki, Shintaro FORORMATION: FORORMATION: FORORMATION: FOR SEQUENCES: FOR SEQUENCES: FOR SEQUENCES: FOR SEQUENCES: FOR SEQUENCES: FOR SECUENCES: FOR S
	5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18       ::::	gn seg 1/1 to: US-08-453-695A-113 from: 1 to: 2347  5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18	block: 5-935-2 x US-08-453-695A-113 5-935-2 x US-08-453-695A-113 from: 1 to: 2347  y 1/1 to: US-08-453-695A-113 from: 1 to: 2347  propropries of the control of t	scores:Quality: 75.50	WCTH: 2347 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear POLE TYPE: cDNA -695A-113 -505A-113 -505A-1	NTION FOR SEQ ID NO: 113:  PROPER SEQ ID NO: 113:  PROPER SEQ ID NO: 113:  Length: 76  Gaps: 4  Gaps: 4  Gaps: 4  Similarity: 61.842 Percent Identity: 32.895  block: 4  Similarity: 61.842 Percent Identity: 32.895  block: 5-935-2 x US-08-453-695A-113  plock: 1.11	LEPHONE: 312/474-6300 LEPTAN: 312/474-6300 LEPTAN: 312/474-6300 LEPTAN: 312/474-6300 VITON FOR SEQ ID NO: 113: NCC CHARACTERISTICS: NCTH: 2347 base pairs PE: nucleic acid RANDEDMESS: single POLOGY: linear STECTCCTAGGCTCCAAGGGTGGATTGGCACCTCCAT 13: Length: 76 Gaps: 4 Similarity: 61.842 Percent Identity: 32.895 block: 6-935-2 x US-08-453-695A-113 FrpTrppheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18 [	IISTRATION NUMBER: 35,302 PERENCE/DOCKET NUMBER: 32658  COMMUNICATION INFORMATION: LEFAX: 312/474-6300 LEXEAX: 312/474-6300 LEXEAX: 312/474-6300 LEFAX: 312/474-6448 LEXEAX: 312/474-6300 LEXEAX: 312/474-6300 LEXEAX: 312/474-6300 LEXEAX: 312/474-6300 ROR SEQ ID NO: 113: ROCE CHARACTERISTICS: ROTH: 2347 base pairs RE: nucleic acid RANDEDNESS: single POLOGY: linear ULE TYPE: CDNA -695A-113 -505CTES: Quality: 75.50 Ratio: 1.606 Ratio:	ASSIFICATION: 530  RNEY/AGENT INFORMATION: #E: No. 5708143 and, Greta E. FISTRATION NUMBER: 35,302 FERENCE/DOCKET NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 LEX: 25-3856 LYION FOR SEQ ID NO: 113: RYION FOR SEQ ID NO: 113: RYION FOR SEQ ID NO: 113: RYION FOR SEQ ID NO: 113: ROTH: 2347 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear FOLOGY: linear	LING DATE: LING DATE: ASSIFICATION: 530 SNEY/AGENT INFORMATION: REY/AGENT INFORMATION: RE: NO. 570814 3and, Greta E. SISTRATION UNUMBER: 32658 COMMUNICATION INFORMATION: LEFAX: 312/474-6300 LEFAX: 312/474-648 LEFAX: 32658 LEFAX:	TWARE: Patentin Release #1.0, Version #1.25  ENT APPLICATION DATA:  LICATION NUMBER: US/08/453,695A  LICATION NUMBER: US/08/453,695A  LICATION NUMBER: US/08/453,695A  LICATION NUMBER: 35,302  SERENCE/DOCKET NUMBER: 35,302  EPHONE: 312/474-6300  LEFAX: 312/474-0448  LEFAX: 312/474-0300  LEPONE: JATA-0448  LEFAX: 312/474-0448  LEFAX: 312/474-0300  LEFAX: 312/474-0448  LEFAX: 312/474-0448  LEFAX: 312/474-0300  LEFAX: 312/474-0448  LEFAX: 313/474-0448  LEFAX: 313/474-0448  LEFAX: 312/474-0448  LEFAX: 32658  LEFAX: 312/474-0448  LEFAX: 312/474-0444  LEFAX: 312/474-044  LEFAX: 312/474-044  LEFAX: 312/474-044  LEFAX: 312/474-044  LEFAX: 312/474-044  LEFAX: 312/474-044  LEFAX: 312	ATUM TYPE: Floppy disk RATING SYSTEM: DC_DOS/MS-DOS RRATING SYSTEM: PC_CDOS/MS-DOS RTAPPLICATION DATA:  DLICATION UNUMBER: 30 RESISTICATION UNUMBER: 35,095A  LING DATE: SSIFICATION: 30 RESISTICATION INFORMATION: 4 RE: NO. 570814 3 and, Greta E.  HISTRATION INFORMATION: 32658  COMMUNICATION INFORMATION: 32658  COMMUNICATION INFORMATION: 1312/474-6300  LEFAX: 312/474-6300  LEFAX: 313::::::::::::::::::::::::::::::::::	TITER READABLE FORM: JUM TYPE: Floppy disk protter: IBM PC compatible REATING SYSTEM: PC DOS/MS-DOS REATING DATA: LLCARION NUMBER: US/08/453,695A JING DATE: SISTRATION NUMBER: 35,302 SISTRATION NUMBER: 35,302 SERENCE/DOCKET NUMBER: 32658 JINGTRATION NUMBER: 32658 JOMMUNICATION INFORMATION: LEFAX: 312/474-0448 LEX: 25-3856 LOMUNICATION FOR SEQ ID NO: 113: RATION FOR SEQ ID NO:	YPE: Illinois NTRY: USA  9: 66506  100	RET: 233 South Wacker, 6300 Sears Tower TY: Chicago TYE: Illinois NTRY: USA 10606 10767 10	RESSEE: Marshall, O'Toole, Gerstein, Murray, 6 RESSEE: Borun RESSEE: Lilinois NTRY: USA NTRY: USA RESSEE: Patentin RESSEE: Patentin Release RATING SYSTEM: PC-DOS/MS-DOS RATING SYSTEM: PC-DOS/MS-DOS RATING SYSTEM: PC-DOS/MS-DOS RATING DATE: RESTORMATION: 530 RESPONSE: Patentin Release #1.0, Version #1.25 RATING DATE: RESPONSE: Patentin Release #1.0, Version #1.25 RESPONSE: PATENTION: S30 RESPONSE: Patentin Release #1.0, Version #1.25 RESPONSE: PATENTION: S30 RESPONSE: NOWBER: 35,302 RESPONSE: 10081 RESPONSE: 312/474-0448 RESPONSE: NOWBER: 35,302 RESPONSE: 25-3856 RESPONSE: S104/474-6300 RESPONSE: 25-386 RESPONSE: S104/474-6300 RESPONSE: RESPONSE: S104/474-6300 RESPONSE: RESPONSE: S104/474-6300 RESPONSE: R	ROF SEQUENCES: 115  SEPONDENCE ADDRESS: SEPONDENCE ADDRESS: SEPONDENCE ADDRESS: SEPONDENCE ADDRESS: SEPONDENCE ADDRESS: RESSEE: Marshall, O'Toole, Gerstein, Murray, & RESPONDENCE ADDRESS: Chicago 100	CANT: Suzuki, Shintaro S OF INVENTION: Protocadherin Materials and Methods ER OF SEQUENCES: 115 SESPONDENCE ADDRESS: SESPONDENCE ADDRESS: SESPONDENCE ADDRESS: Chicago 105	51 pSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheS 65 :::::::  :::  :::  :::  :::  :::  ::
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SISTRARION NUMBER: 35,302 SISTRARION NUMBER: 35,302 SERNCE/DOCKET NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 LEX: 25-3856 AVION FOR SEQ ID NO: 113: NTON FOR SEQ ID NO: 113: NTON FOR SEQ ID NO: 113: NTON FOR SEQ ID NO: 113: STOLE TYPE: CDNA C695A-113  SCOICES: Quality: 75.50 Ratio: 1.606 Ratio: 1.606 Similarity: 61.842 Percent Identity: 32.895 Lblock: 5-935-2 x US-08-453-695A-113 from: 1 to: 2347  J1/1 to: US-08-453-695A-113 from: 1 to: 2347  g1/1 to: US-08-453-695A-113 from: 1	LING DATE: LING DATE: ASSIFICATION: 530 ASSIFICATION: 530 ASSIFICATION: 530 ASSIFICATION: 530 ASSIFICATION: 530 ANEY, AGENT INFORMATION: BE: NO. 570814 3 and, Greta E. 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LISTRATION NUMBER: 35,302  LEPHONE: 312/474-0348  LEX: 25-3856  LOMMUNICATION INFORMATION:  LEPHONE: 312/474-0448  LEX: 25-3856  LOMMUNICATION INFORMATION:  LEPHONE: 312/474-0448  LEX: 25-3856  LOMBER: 32/474-0448  LEX: 25-3856  LEPHONE: 312/474-0448  LEX: 25-3856  LOMBER: 32/474-0448  LEX: 25-3856  LEPHONE: 312/474-0448  LEX: 25-3856  LOMBER: 32/474-0448  LEX: 25-3856  LOMBER: 32/474-0448  LEX: 37/474-0448  LEX: 32/474-0448  LEX: 25-3856  LEPHONE: 32/474-0448  LEX: 37/474-0448  LEX: 32/474-0448  LEX: 37/474-0448  LEX: 32/474-0448  LEX: 32/474-	TITER READABLE FORM: DIUM TYPE: Floppy disk proter: IBM PC compatable proter: IIBM PC compatable proter: IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	YPE: Illinois NTRY: USA P: 60606 PTORER READABLE FORM: JUM TYPE: Floppy disk RUTER: IBM PC compatible RRATING SYSTEM: PC-DOS/MS-DOS PTWARE: Patentin Release #1.0, Version #1.25 PRATING SYSTEM: PC-DOS/MS-DOS PTWARE: Patentin Release #1.0, Version #1.25 PRATING SYSTEM: PC-DOS/MS-DOS PTWARE: Patentin Release #1.0, Version #1.25 PRATING SYSTEM: PC-DOS/MS-DOS PTWARE: Patentin Release #1.0, Version #1.25 PTOS STITION: 530 NOTE OF SEQ IN THE PROPERTION: REPHONE: 31/474-0448 LEX: 25-3856 COMMUNICATION INFORMATION: REPHONE: 31/474-0300 LEFAX: 31/474-0448 LEX: 25-3856 COMMUNICATION INFORMATION: REPHONE: 31/4-0448 LEX: 25-3856 COMMUNICATION INFORMATION: REPHONE: 31/4-0448 LEX: 25-3856 COMMUNICATION INFORMATION: REPHONE : 32/47-0448 LEX: 25-3856 COMMUNICATION INFORMATION: REPHONE : 13: 11/4 LEPHONE: 32/47-0448 LEX: 105-08-453-695A-113 Length: 76 Gaps: 4 Similarity: 61.842 Percent Identity: 32.895 Length: 76 Gaps: 4 Similarity: 61.842 Percent Identity: 32.895 Length: 76 Gaps: 4 Similarity: 61.842 Percent Identity: 32.895 Length: 76 Gaps: 4 Similarity: 61.842 Percent Identity: 32.895 Length: 76 Gaps: 4 Similarity: 76 Gaps: 4 Sim	REFI: 233 South Wacker, 6300 Sears Tower TY: Chicago NTRY: USA DIOM TYPE: Illinois JIER READABLE FORM: JIER READABLE FORM: JUMN TYPE: Floppy disk APUTER: IBM PC compatible REATING SYSTEM: PC DOS/MS-DOS STWARE: Patentin Release #1.0, Version #1.25 SHATANG SYSTEM: PC DOS/MS-DOS STWARE: Patentin Release #1.0, Version #1.25 SHATANG SYSTEM: PC DOS/MS-DOS STWARE: Patentin Release #1.0, Version #1.25 SHATANG NUMBER: US/08/453,695A JING DATE: SSIFICATION NUMBER: 330 SISTRATION NUMBER: 33058 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 JISTRATION NUMBER: 33658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 JISTRATION NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 JISTRATION NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 JISTRATION NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-0448 JISTRATION: 530 LEPHONE: 32658 COMMUNICATION INFORMATION: LEPHONE: 1013: LEPHONE: 102/474-0448 JISTRATION: 102/474-0448 JISTRATION: 102/474-0448 JISTRATION: 102/474-0448 JISTRATION: 113: LEPHONE: 102/474-0448 JISTRATION: 113: LEPHONE: 32658 LONGER MADERION: 113: LEPHONE: 102/474-0448 JISTRATION: 113: LEPHONE: 102/47-0448 JISTRATION: 113: LEPHONE: 102/47-0448 JISTRATION: 113: LEPHONE: 102/47-0448 JISTRATION: 113: LEPHONE: 102/47-0448 JISTRATION: 125 LEPHONE: 102/47-0448 JISTRATION: 125 LEPHONE: 126 LEPHONE: 1	NESSEE: Marshall, O'Toole, Gerstein, Murray, & REESSEE: Borun (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	ROF SEQUENCES: 115 SPONDENCE ADDRESS: SPONDENCE ADDRESS: SPONDENCE ADDRESS: Chicago VTE: Illnois NTRY: USA Chicago NTRY Chica	CANT: Sužuki, Shintaro S OF INVENTION: Protocadherin Materials and Methods ER OF SEQUENCES: 115 SESPONDENCE ADDRESS: 155 SESPONDENCE ADDRESS: 157 SEST: 233 South Wacker, 6300 Sears Tower FY: Chicago TYE: Illinois NITRY: USA PITER READABLE FORM: FIGHER STEM: PC-DOS/MS-DOS PYARE: IBM PC Compatible PRATING SYSTEM: PC-DOS/MS-DOS PYARE: IBM PC Compatible PRATING SYSTEM: PC-DOS/MS-DOS PYARE: DATA: SULCATION NUMBER: 35,302 SETENCE/DOCKET NUMBER: 35,302 SETENCE/DOCKET NUMBER: 35,302 SETENCE/DOCKET NUMBER: 32658 VION TON: 570814 3and, Greta E. SISTRATION UNMBER: 32,300 SEFAX: 312/474-0448 SETENCE/DOCKET NUMBER: 32658 VION FOR SEQ ID NO: 113: SCOTES: 25-3856 VION FOR SEQ ID NO: 113: SCOTES: 25-3857 CCS SCTH: 2347 base pairs DLEFAX: 211 base pairs SED CHARACTERISTICS: SCTH: 2347 base pairs SCTH: 2347 b	GlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyAs 51           :::
GlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyAs 51  GTCTCGCCAGCTCCAGGGCTCCAAAGGTGGATTGGCTCCTGCACCTCCAT 132  pSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheS 65  :::::   :::	5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18	gn seg 1/1 to: US-08-453-695A-113 from: 1 to: 2347  5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18	_block: 5-935-2 x US-08-453-695A-113  j 1/1 to: US-08-453-695A-113 from: 1 to: 2347  j 1/1 to: US-08-453-695A-113 from: 1 to: 2347  IIPTTPPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18       :::      :::   IIIITTPPHEALATYRLEU	Quality: 75.50  Quality: 75.50  Ratio: 1.606  Ratio: 1.606  Similarity: 61.842  Percent Identity: 32.895  block: 5-935-2 x US-08-453-695A-113  J/1 to: US-08-453-695A-113 from: 1 to: 2347  graphealaTyrLeuLeuThrSerIleIleLeuThrLe 18	WCTH: 2347 base pairs  BE: nucleic acid  RANDEDNESS: single  POLOGY: linear  SCORES: 75.50  Quality: 75.50  Ratio: 1.606  Ratio: 1.606  Ratio: 1.606  Similarity: 61.842  Percent Identity: 32.895  block:  5-935-2 x US-08-453-695A-113  1/1 to: US-08-453-695A-113 from: 1 to: 2347  grpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18	MION FOR SEQ ID NO: 113:  SECORES:  QUALITY: 75.50  Quality: 75.50  Ratio: 1.606  Ratio: 1.606  Matio: 1.606  Factio: 1.606  Matio: 1.606  Matio: 1.606  Matio: 1.608  Matio: 1.606  Matio	LEPHONE: 312/474-6300 LEPHAN: 312/474-6300 LEPHAN: 312/474-6300 LEX: 25-3856 NTION FOR SEQ ID NO: 113: NTION FOR SEQ ID NO: 113: NGCE CHARACTERISTICS: NGTH: 2347 base pairs PE: nucleic acid POLOGY: linear POLOGY: linear NULE TYPE: CDNA -695A-113  -scores: Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Partiy: 61.842 Percent Identity: 32.895  block: -5-335-2 x US-08-453-695A-113 J/1 to: US-08-453-695A-113 ILPTTPPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18        :::	IISTRATION NUMBER: 35,302 PERRENCE/DOCKET NUMBER: 32658  COMMUNICATION INFORMATION: LEFAX: 312/474-0448  LEFAX: 312/474-0448  LEFAX: 312/474-0448  LEFAX: 312/474-0448  LEFAX: 312/474-0448  LEFAX: 312/474-0448  LEFAX: 312/474-048  ANDEDNES: SINGLE NO: 113: ROCE CHARACTERISTICS: PE: nucleic acid RANDEDNESS: single POLOGY: 11near  ULE TYPE: cDNA -695A-113  -guality: 75.50	ASSIFICATION: 530  NEY/AGENT INFORMATION: 4E: No. 5708143and, Greta E. SISTRAPION NUMBER: 35,302 SISTRAPION NUMBER: 32658  COMMUNICATION INFORMATION: LEFAX: 312/474-6408 LEFAX: 312/474-6408 LEFAX: 312/474-6300 LEFAX: 312/474-6	LING DATE: LING DATE: ASSIFICATION: 530  NEWLYACENT INFORMATION: ASSIFICATION: 530  NEWLYACENT INFORMATION: AS: NO. 570814 3and, Greta E. SISTRATION UNUMBER: 35,302 SERENCE/DOCKET NUMBER: 32658 COMMUNICATION INFORMATION: LEPAN: 312/474-0448 LEX: 25-3856 VION FOR SEQ ID NO: 113: ENCE CHARACTERISTICS: WOTH: 2347 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear ULE TYPE: CDNA -695A-113  -scores: Quality: 75.50 Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Similarity: 61.842 Percent Identity: 32.895  block: 5-935-2 x US-08-453-695A-113  block: 5-935-2 x US-08-453-695A-113 from: 1 to: 2347  J1/1 to: US-08-453-695A-113 from: 1 to: 2347	TWARE: Patentin Release #1.0, Version #1.25 ENT APPLICATION DATA: LLCATION NUMBER: US/08/453,695A LICATION NUMBER: US/08/453,695A LICATION NUMBER: US/08/453,695A LICATION NUMBER: US/08/453,695A LETANTON NUMBER: 35,302 ENEMONICATION INFORMATION: LEFAN: 312/474-0300 LEFAX: 312/474-0300 LEFAX: 312/474-0448 LEY: 25-3856 ANION FOR SEQ ID NO: 113: ENCE CHARACTERISTICS: MICHICAL COLOR LEFAX: 312/474-0448 LEY: 2347 base pairs DE: nucleic acid ANDEDMESS: single OLOGY: linear ULE TYPE: CDNA -695A-113 -scores: -guality: 75.50 Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Similarity: 61.842 Percent Identity: 32.895 block: -block: -5-935-2 x US-08-453-695A-113 INTITYPPheAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPheAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPheAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPHEAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPHEAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPHEAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPHEAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPHEAlaTyrLeuLeuThrSerIleIleLeuThrLe RIPTTPPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleLeuThrLe RIPTTPHEALATYLEULeuThrSerIleIleUThrLe RIPTTPHEALATYLEULeuThrSerIleIleUThrLe RIPTTPHEALATYLEULeuThrSerIleIleUThrLe RIPTTPHEALATYLEULeuThrSerIleIleUThrLe RIPTTPHEALATYLEULeuThrSerIleIleUThrLe RIPTTPHEALATYLEULeuThrSerIle RIPTTPHEALATYLEULeuThrSerIle RIPTTPHEALATYLEULeuThrSerIle RIPTTPHEALATYLEU	ATUM TYPE: Floppy disk RATING SYSTEM: PC Compatible RRATING SYSTEM: PC COMPATION RRATING SYSTEM: PC COMPATION RRATING SYSTEM: PC COMPATION RE: PAICHTION DATA: LICATION NUMBER: US/08/453,695A LIGHTON INFORMATION: AND 570814 3and, Greta E. HISTRATION INFORMATION: LEPHONE: 312/474-6300 LEFAX: 312/474-6300 LEFAX: 312/474-0448 LEX: 25-3856 WIGN FOR SEQ ID NO: 113: EMPHONE: 312/474-048 LEX: 25-3856 WIGN FOR SEQ ID NO: 113: SNCE CHARACTERISTICS: WCTH: 2347 base pairs RANDEDNESS: single POLOGY: linear ULE TYPE: CDNA -695A-113 -scores: Quality: 75.50 RRILO: 1.606 RRILO: 1.606 Similarity: 61.842 Percent Identity: 32.895 block: block: 5-335-2 x US-08-453-695A-113 from: 1 to: 2347 J1/1 to: US-08-453-695A-113 from: 1 to: 2347 INFTTPPheAlaTyrLeuLeuThrSerIleIleLeuThrLe RGGTGGTGGGCAGTGGCTGTGGTCTCCTTGTCATT 123	JIUM TYPE: Floppy disk JIUM TYPE: Floppy disk PUTER: IBM PC compatible RATING SYSTEM: PC-DOS/MS-DOS RATING DATE:  NITERICATION NUMBER: 35,302 STERENCE/DOCKET NUMBER: 35,302 STERENCE/DOCKET NUMBER: 35,302 LEFAN: 312/474-0448 LEFAX: 312/474-0448 LEFAX: 312/474-0448 LEFAX: 312/474-0448 LEFAX: 312/474-0448 LEY: 25-3856 ATION FOR SEQ ID NO: 113: ROCE CHARACTERISTICS: ROTH: 2347 base pairs PC: nucleic acid RANDEDMSS: single POLOGY: linear DOLOGY: lin	YPE: Illinois NTRY: USA 2: 60606 7: 60606 7: 60606 7: 60606 7: 60606 7: 60606 7:	REFI: 233 South Wacker, 6300 Sears Tower TRE: 111inois NTRY: USA NTRY: USA 15: 60606 1FER READABLE FORM: 11UM TYPE: Floppy disk PUTER: IBM PC compatible RATING SYSTEM: PC-DOS/MS-DOS PTWARE: Patentin Release #1.0, Version #1.25 PTWARE: Patentin Re	RESSEE: Borun  REST: 23 South Wacker, 6300 Sears Tower  YE: Chicago  YIE: Illinois  NITRY: USA  PIER READABLE FORM:  PIER READABLE FORM:  PIER READABLE FORM:  POLOGYMS-DOS  RATING SYSTEM: PC-DOS/MS-DOS  RATING SYSTEM: PC-DOS/MS-DOS  NEWY/REI DATE:  NEWY/REI IBM PC Compatible  REFICATION NUMBER: US/08/453,695A  LICATION NUMBER: US/08/453,695A  LICATION NUMBER: 35,302  SISTRATION NUMBER: 35,302  SERENCE/DOCKET NUMBER: 35,302  SERENCE/DOCKET NUMBER: 3658  COMMUNICATION INFORMATION:  LEFAX: 312/474-0304  LEFAX: 312/474-0448  LEFAX:	ROP SEQUENCES: 115 SEPONNDENCE ADDRESS: SEPONDENCE ADDRESS: RESSEE: Marshall, O'Toole, Gerstein, Murray, & RESSEE: Marshall, O'Toole, Gerstein, Murray, & RESSEE: Borun REET: 233 South Wacker, 6300 Sears Tower PY: Chicago YTE: Illnois NTRY: USA 2: 60506  JIER READABLE FORM: JUN TYPE: Floppy disk PUTER: IRD PC compatible REATING SYSTEM: PC-DOS/MS-DOS FRATING SYSTEM: PC-DOS/MS-DOS FRATING SYSTEM: PC-DOS/MS-DOS REY/AGENT INFORMATION: SSIFICATION NUMBER: 35,302 PERENCE/DOCKET NUMBER: 35,302 PERENCE/DOCKET NUMBER: 32,505 PERENCE/DOCKET NUMBER: 32	COANT: Suzuki, Shintaro  OF OF ENQUENCES: 115  SPONDENCE ADDRESS: SPONDENCE: 23 South Wacker, 6300 Sears Tower PY: Chicago STERIC 23 South Wacker, 6300 Sears Tower PY: Chicago STERIC 23 South Wacker, 6300 Sears Tower PY: Chicago STERIC 25	18 uSer.ProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHis 34
user.ProGlySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHis 34		gn seg 1/1 to: US-08-453-695A-113 from: 1 to: 234	block: 5-935-2 x US-08-453-695A-113 3 1/1 to: US-08-453-695A-113 from: 1 to: 234	Scores: 75.50 Length: 76 Quality: 75.50 Length: 76 Ratio: 1.606 Gaps: 4 Similarity: 61.842 Percent Identity: 32.895 block: 5-935-2 x US-08-453-695A-113 3 1/1 to: US-08-453-695A-113 from: 1 to: 234	WCTH: 2347 base pairs PE: nucleic acid RANDEDNESS: single POLOGY: linear SULE TYPE: cDNA -695A-113 -scores: Quality: 75.50 Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Similarity: 61.842 Percent Identity: 32.895 block: block: 5-935-2 x US-08-453-695A-113 J/1 to: US-08-453-695A-113 from: 1 to: 234	MION FOR SEO ID NO: 113:  NYTON FOR SEO ID NO: 113:  NOTH: 2347 base pairs  WETH: 2347 base pairs  WETH: 2347 base pairs  DE: nucleic acid RANDEDNESS: single  POLOGY: linear  ULLE TYPE: cDNA  -695A-113  -695A-113  -scores: Quality: 75.50 Ratio: 1.606 Ratio: 1.606 Ratio: 1.606 Similarity: 61.842 Percent Identity: 32.895  block: 5-935-2 x US-08-453-695A-113  1/1 to: US-08-453-695A-113 from: 1 to: 234	LEPHONE: 312/474-6300  LEFAX: 312/474-6300  MION FOR SEQ ID NO: 113:  NOTH: 2347 base pairs  NOTH: 2347 base pairs  ENCE CHARACTERISTICS:  WOTH: 2347 base pairs  ENCE CHARACTERISTICS:  WOTH: 2347 base pairs  PROLOGY: linear  ULL TYPE: cDNA  -095A-113  SCORES: Quality: 75.50  Ratio: 1.606  Ratio: 1.606  Similarity: 61.842 Percent Identity: 32.895  block: CDNA  1/1 to: US-08-453-695A-113 from: 1 to: 234	### STRATION NUMBER: 35,302 ### STRENCE/DOCKET NUMBER: 32658 **DOMMUNICATION INFORMATION: **LEFAX: 312,474-6300 **LEFAX: 25-3856 **LIST 25-3856 **LIST 25-3856 **LIST 25-2856 **LIST 247 base pairs **LOTH: 2347 base pairs **LOTH: 2348 b	ASSIFICATION: 530 ANEY/AGENT INFORMATION: #E: NO. 5708143and, Greta E. SISTRARION NUMBER: 35,302 SISTRARION NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-6300 LEPAX: 312/474-0448 LEX: 25-3856 AVION FOR SEO ID NO: 113: AVION FOR FOR SEO ID NO: 113: AVION FOR SEO ID NO: 113: AVION FOR SEO ID N	LICATION UNMEER: US/08/453,695A  ASSIFICATION: 530  NEY/ACENT INFORMATION: HE: NO. 570814 3and, Greta E. HISTRATION NUMBER: 35,302 FERENCE/DOCKET NUMBER: 32658  COMMUNICATION INFORMATION: EPHONE: 312/474-6300 LEFAX: 312/474-0448  ATTON FOR SEQ ID NO: 113: NOE CHARACTERISTICS: NOE CHARACTERISTICS: NOTH: 2347 base pairs F: nucleic acid ARNDEDMESS: single POLOGY: linear CHARACTERISTICS: OLOGY: linear CHARACTERISTICS: SINGLE CDNA  -895A-113  -905A-113  -9010GY: linear CHARACTERISTICS: OLOGY: lin	TWARE: Patentin Release #1.0, Version #1.25 EMT APPLICATION DATA:  LICATION NUMBER: US/08/453,695A  LICATION NUMBER: US/08/453,695A  ASSIFICATION: 530 ANEY/ACENT INFORMATION: ANEY/ACENT INFORMATION: BERENCE/DOCKET NUMBER: 35,302 EFRENCE/DOCKET NUMBER: 3658  COMMUNICATION INFORMATION: LEFAX: 312/474-6300 LEFAX: 312/474-6448  LEFAX: 312/474-0448  LEFAX: 312/474-0448  LEFAX: 312/474-6300  LEFAX: 32/474-6300  LEFAX: 312/474-6300	ATUM TYPE: Floppy disk REVITER: IBM PC COMPATABLE RRATING SYSTEM: PC CDOS/MS-DOS PTWARE: Patentin Release #1.0, Version #1.25 PTWARE: PATENTION NUMBER: US/08/453,695A PTWARE: STORMATION: PERSONCET NUMBER: 35,302 PERSONCET NUMBER: 35,302 PERSONCET STORMATION: PERSON: 312/47-0448 PERSONCE CHARACTERISTICS: WITON FOR SEQ ID NO: 113: PUBLISTER STORMATION: PERSON IN STORMATI	TITER READABLE FORM: DIUM TYPE: Floppy disk proter: IBM PC compatible RATING SYSTEM: PC-DOS/MS-DOS RATING SYSTEM: PC-DOS/MS-DOS RATING SYSTEM: PC-DOS/MS-DOS RATING DATE: STARPLICATION NUMBER: US/08/453,695A LING DATE: SSIFICATION NUMBER: 3500 ANEY/AGENT INFORMATION: ANEY/AGENT INFORMATION: ANEY/AGENT INFORMATION: SISTRARION NUMBER: 32658 COMMUNICATION INFORMATION: LEPHONE: 312/474-6300 LEPHONE	TYP: (Chicago NTRY: USA  10606 10766 10767 10772 1087 1087 1087 1087 1087 1087 1087 1087	REFI: 233 South Wacker, 6300 Sears Tower REFI: 211inois NTRY: USA TYPE: Illinois TYPE READABLE FORM: THE READABLE FORM: THE READABLE FORM: THE READABLE FORM: THE PACTORY OF THE PROPERTING SYSTEM: PC-DOS/MS-DOS TWARE: Patentin Release #1.0, Version #1.25 THARTING SYSTEM: PC-DOS/MS-DOS TWARE: Patentin Release #1.0, Version #1.25 THARTING SYSTEM: PC-DOS/MS-DOS TWARE/AGENT INFORMATION: ANEY/AGENT INFORMATION: ANEY/AGENT INFORMATION: ANEY/AGENT INFORMATION: SISTRARION NUMBER: 35.302 THERMOLOFIC NOINFORMATION: ANEY/AGENT NUMBER: 32658 TOMMUNICATION INFORMATION: LEPHONE: 312/474-6300 LEPHONE: 312/474-6488 LEX: 25-3856 TAYION FOR SEO ID NO: 113: ANION FOR	RESSEE: Marshall, O'Toole, Gerstein, Murray, RESSEE: Borun RESSEE: Borun RESSEE: Boun Yre: Chicago Yre: Ilinois NTRY: USA 2: 60606 PIFER READABLE FORM: PC-DOSYMS-DOS RATING SYSTEM: PC-DOSYMS-DOS RATING NUMBER: US/08/453,695A LING DATE: LICATION NUMBER: US/08/453,695A LING DATE: PLICATION NUMBER: 330 RATY/ACENT INFORMATION: RESPANCIAL NUMBER: 35,302 FERENCE/DOCKET NUMBER: 32,302 FERENCE/DOCKET NUMBER: 32,302 FERENCE/DOCKET NUMBER: 32,302 LEFAX: 312/474-6300 LEFAX: 312/474-6300 LEFAX: 312/474-6300 LEFAX: 312/474-6448 LEX: 25-3856 MINION FOR SED ID NO: 113: RCC CHARACTERISTICS: ROTH: 2347 base pairs POLOGY: linear ULE TYPE: CDNA -695A-113 -SCORES: Quality: 75.50 Ratio: 1.606 Ratio: 1.606 Similarity: 61.842 Percent Identity: 32.895 block: 5-935-2 x US-08-453-695A-113 LC 234	ROF SEQUENCES: 115 SEPONNENCE ADDRESS: 115 SEPONNENCE ADDRESS: 115 SEPONNENCE ADDRESS: 23 South Wacker, 6300 Sears Tower PY: Chicago ATE: 11inois NMTRY: USA POTER READABLE FORM: DION TYPE: Floppy disk PUTER: IBM PC compatible PC-DOS/MS-DOS PWARE: PATENTION: 5708145710N: 530 NNEY/ACENT INFORMATION: 530 NNEY/ACENT INFORMATION: 5708143 and, Greta E. SISTRATION NUMBER: 35,302 STERENCE/DOCKET NUMBER: 35,302 STERENCE/DOCKET NUMBER: 32658 COMMUNICATION INFORMATION: LEFAX: 312/474-0448 LEFAX: 312/474-030 LEFAX: 312	CANT: Suzuki, Shintaro  E OF INVENTION: Protocadherin Materials and  ER OF SEQUENCES: 115  SEPONDENCE ADDRESS:  SEPONDENCE ADDRESS:  Marshall, O'Toole, Gerstein, Murray  RESSEE: Marshall, O'Toole, Gerstein, Murray  RESSEE: Marshall, O'Toole, Gerstein, Murray  REST: 233 South Wacker, 6300 Sears Tower  TY: Chicago  TYE: Illinois  NTRY: USA  10606  PERATING SYSTEM: PC-DOS/MS-TOS  PWARE: Ploppy disk  APPLICATION NUMBER: US/08/453,695A  ING DATE:  SSIFICATION NUMBER: US/08/453,695A  ING DATE:  SSIFICATION NUMBER: US/08/453,695A  ING DATE:  SSIFICATION NUMBER: 335,302  SITORAPION NUMBER: 35,302  SITORAPION NUMBER: 35,302  SITORAPION NUMBER: 35,302  SEPHONE: 312/474-0448  EX: 25-3856  COMMUNICATION INFORMATION:  LEPHONE: 312/474-0448  EX: 25-3856  SMION FOR SEQ ID NO: 113:  MION FOR SEQ ID NO: 113:  SOURCE CHARACTERISTICS:  SOTH: 2347 base pairs  DILETYPE: CDNA  -695A-113  -500A-113  -500A-113  -500A-113  -500A-113  -500A-113  -500A-113  -600A-113  -600A-113  -701A-100A-100A-100A-100A-113  -701A-100A-100A-100A-113  -701A-100A-100A-113  -701A-100A-100A-113  -701A-100A-100A-113  -701A-100A-100A-113  -701A-100A-100A-113  -701A-100A-113  -701A-100A-100A-113  -701A-100A-100A-100A-113  -701A-100A-100A-100A-113  -701A-100A-100A-100A-100A-113  -701A-100A-100A-100A-100A-100A-100A-100A	5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLe 18
CANT: Suzuki, Shintaro CANT: Suzuki, Shintaro CANT: Suzuki, Shintaro CANT: Suzuki, Shintaro R OF INVENTION: Protocadherin Materials and Methods R OF SEQUENCES: 115 RESSEE: Marshall, O'Toole, Gerstein, Murray, & RESSEE: Borun PRESSE: Borun RESSE: Borun RESSE: Borun RESSE: Borun RESSE: Borun RESSE: Borun RESSE: Borun RESTATION SUBMER RESPONDER: IBM PC Compatible RETTING SYSTEM: PC-DOS/MS-DOS RETTING NUMBER: 33,302 SHICATION DATA: 35,302 RES NO. 5708143 and, Greta E. RE: NO. 5708145 a	LINFORMATION: INFORMATION: INFORMATION: CANT: Suzuki, Shintaro GOFINVENTION: Protocadherin Materials and SPONDENCE ADDRESS 115 SET 233 South Wacker, 6300 Sears Tower TY: Chicago TYE: Ilinois NTRY: USA SUIM TYPE: Floppy disk JUM TYPE: JUM TYPE: JUM JUM JUM TYPE: JUM	Patent No. 5708143 GENERAL INFORMATION: APPLICANW: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illnois COUNTRY: USA ZIP: 60606 COMPUTER EADDRELE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.25 COMPUTER: IBM PC COMPATION: APPLICATION NUMBER: US/08/453,695A FILING DATE: CLASSIFICATION STATA: APPLICATION NUMBER: US/08/453,695A FILING DATE: CLASSIFICATION INFORMATION: APPLICATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 32,302 REFERENCE/DOCKET NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 32658 TELEPHONE: 312/474-0448	Patent No. 5708143 GENERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/453,695A FILING DATE: CLASSIFICATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 37,305 TELEFAX: 312/474-0448 TELEFAX: 312/474-0448 TELEFAX: 312/474-0448 TELEFAX: 312/474-0448 INFORMATION FOR SEQ ID NO: 113: SEQUENCE CHARACTERISTICS: LENGTH: 2347 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA 15-08-453-695A-113	Patent No. 5708143 GENERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60506 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: PATENTION NATA: APPLICATION NUMBER: US/08/453,695A FILING DATE: CLASSIFICATION UMBER: US/08/453,695A FILING DATE: NAME: No. 5708143and, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 33658 TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-0448 INFORMATION FOR SEQ ID NO: 113:	Patent No. 5708143 GEMERAL INFORMATION:    APPLICANT: SUZUKI, Shintaro    TITLE OF INVENTION: Protocadherin Materials and    NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS:    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray    ADDRESSEE: Borun    STREET: 233 South Wacker, 6300 Sears Tower    CITY: Chicago    STATE: Illinois    COUNTRY: USA    ZIP: 60606 COMPUTER READABLE FORM:    MEDIUM TYPE: Floppy disk    COMPUTER: IBM PC compatible    OPERATING SYSTEM: PC-DOS/MS-DOS    SOFTWARE: Patentin Release #1.0, Version #1.25    SOFTWARE: Patentin Release #1.0, Version #1.25    CLASSIFICATION: 530    ATTORNEY/AGENT INFORMATION:    NAME: No. 5708143and, Greta E.    REGISTRATION UNMBER: 35,302    REFERENCE/DOCKET NUMBER: 32658    TELECOMMUNICATION INFORMATION:    TELEPHONE: 312/474-0448    TELEPHONE: 312/474-0448	Patent No. 5708143 GEMERAL INFORMATION: GEMERAL INFORMATION: GEMERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/453,695A FILING DATE: CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: No. 5708143and, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 32658	Patent No. 5708143 GEMERAL INFORMATION:    APPLICANT: SUZUKI, Shintaro    TITLE OF INVENTION: Protocadherin Materials and    NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS:    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray    ADDRESSEE: Borun    STREET: 233 South Wacker, 6300 Sears Tower    CITY: Chicago    STATE: Illinois    COUNTRY: USA    ZIP: 60606 COMPUTER: EADDABLE FORM:    MEDIUM TYPE: Floppy disk    COMPUTER: IBM PC compatible    OPERATING SYSTEM: PC-DOS/MS-DOS    SOFTMARE: PAtentin Release #1.0, Version #1.25    SOFTMARE: DATE:    CLASSIFICATION NUMBER: US/08/453,695A    FILING DATE:    CLASSIFICATION: 530    ATTORNEY/AGENT INFORMATION:    NAME: NO. 5708143 and. Greta E.	Patent No. 5708143 GENERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois COUNTRY: USA ZID: 60506 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/453,695A FILING DATE:	Patent No. 5708143 GEMERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: 1111nois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ITM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Release #1.0, Version #1.25	Patent No. 5708143 GEMERAL INFORMATION:    APPLICANT: SUZUKI, Shintaro    TITLE OF INVENTION: Protocadherin Materials and    NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS:    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray    ADDRESSEE: Borun    STREET: 233 South Wacker, 6300 Sears Tower    CITY: Chicago    STATE: Illinois    COUNTRY: USA    ZIP: 60606 COMPUTER: ISA PC compatible    COMPUTER: IBM PC compatible	Patent No. 5708143 GENERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray ADDRESSE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM:	Patent No. 5708143 GENERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois COUNTRY: USA	Patent No. 5708143 GENERAL INFORMATION: APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 233 South Wacker, 6300 Sears Tower	Patent No. 5708143  GENERAL INFORMATION: APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115  CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Marshall, O'Toole, Gerstein, Murray	Patent No. 5708143 GENERAL INFORMATION: APPLICANT: SUZUKI, Shintaro TITLE OF INVENTION: Protocadherin Materials and NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS:	Patent No. 5708143  GENERAL INFORMATION: APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocadherin Materials and	INFORMATION:		

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## ALIGNMENTS

A;Cross-references: GB:AE000458; GB:U00096; NID:g2367299; PIDN:AAC76827.1; PID:g17902 A;Experimental source: strain K-12, substrain MG1655 R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R. Science 257, 771-778, 1992 A;Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84. A;Reference number: S30660; MUID:92358234 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617 A;Accession: A65187 R; Blattner, F.R.; Plunkett III, A.; Rose, D.J.; Mau, B.; Shao, Science 277, 1453-1462, 1997 C;Species: Escherichia coli C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 08-Oct-1999 C;Pacession: A65187; S30714 밁 Qy 멍 A;Status: nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 'V',2-138 <DAN> A;Cross-references: EMBI:M87049 A;Note: the nucleotide sequence was submitt Ωy Qy hypothetical 15.4 kD protein in recQ-pldB intergenic region - Escherichia coli (strai N;Alternate\_names: hypothetical protein f138 A; Molecule type: DNA A; Residues: 1-138 <BLAT> A; Accession: S30714 A; Status: preliminary; nucleic acid sequence Query Match Best Local S Matches 121 188 128 61 Local Similarity FGSLFMLVGALLASARHA 205 LAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALWIKGPKQMKALNKI 120 LAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALMIKGPKQMKALNKI 187 FGSLFMLVGALLASARHA 138 Conservative EMBL:M87049 ide sequence was submitted to 64.7%; 99.3%; G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Y. Score 686; DB 2; Pred. No. 5.7e-58; 1; Mismatches 0 translation not shown; translation the 0; Length 138; EMBL Data Library, November Indels not shown 0; not shown Gaps 0; 1992

nypothetical prote

RESULT G82358

conserved hypothetical protein VC0136 [imported] - Vibrio cholerae (group Ol strain

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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_c
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_c
C;Accession: C82990
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginos
A;Reference number: A82950; MUID: 20437337
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C;Date: 18-B-358
C;Accession: G82358
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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A:Residues: 1-205 (HEI)
A:Cross-references: GB:AE004104;
A:Experimental source: serogroup
C:Genetics:
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A;Molecule type: DNA
A;Residues: 1-209 <STO>
A;Cross-references: GB:AE004937; GB:AE004091; NID:g9951553; PIDN:AAG08634.1;
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A;Map position: 1
C;Superfamily: hypothetical protein b1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PA5249 [imported] - Pseudomonas aeruginosa (strain
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Gene: PA5249
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Best Local Similarity
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Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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    59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIMTRMNKLFGSMFMGCGMLLATAK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTNPKSIVELAALEPQEIMPQQPQLMQYIVLGVTTIVVDIIVMIGVATLAQRIALWIKGP 178
                                             MLVSTWFAFFLACWAISLSPGAGAIASMSCGLQYGFARG----
                                                                                MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTNPKSIVFLVALFPQFIDPTRDHWPQFLVLGITTVTIDAIVMFGYTALAAQLGRYIRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIGALVAQSALAFTLIKWIGAAYLVWLGIQKWRDRAPLTATTTSHELSQAALLRKAVLIN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDIHVWLAYLLTAVVFSLAPGSGTVNSISNGLSYGTRHSLGAIIGLQIGLACHIVLVG-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHG--YPAGGVYCWASDRTGDSYCAGWR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
-GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLAS 103
                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of Pseudomonas aeruginosa PA01,
50; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.3%;
                                                                                                                                                    36.7%; Score 389; DB 2; 36.4%; Pred. No. 1.2e-29;
                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AE003852; NID:g9654534; Ol; strain N16961; biotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 459.5; DB 2; Pred. No. 2.5e-36;
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                         Length 209;
                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.R.; Kas,
                                           ----YWNAL 44
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El Tor
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                                                                                    58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hickey,
Larbig,
                                                                                                                                                                                                                                                                                                         GSPDB:GN00
                                                                                                                                4;
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K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                          path
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hypothetical protein b1798 - Escherichia coli (strain K-12) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_ch C;Accession: F64940 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T. Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
                                      A; Molecule type: DNA
A; Residues: 1-212 <BLAT>
                                                                                          A;Title: The complete genome sequence of Escherichia coli K-12 A;Reference number: A64720; MUID:97426617 A;Accession: F64940
                                                                                                                                                                                                                                                                                                                                                                           밁
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A;Molecule type: A;Molecule type: L-241 <WHI>
A;Residues: 1-241 <WHI>
A;Cross-references: GB:AE002038; GB:AE000513; NID:g6459790; PIDN:AAF11548.1; PID:g645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE000274;
                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , M.; Shen, M.; Vamathevan, J.J.; Lam, S.; Smith, H.O.; Venter, J.C.; Fraser, Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δõ
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                                                                                                                                                                                                                                                                                                 F64940
                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A75250; MUID:20036896
A;Accession: C75329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                                                                174 WIKG-PKQMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 IIVMIGYATLAQRIALWIKGPKQMKALNKIFGSLFMLVGALLASARHA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
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                                                                                                                                                                                                                                                                                                                                                                           RLQGNPRFQRGQKVASGGAMIALGTYVAVER 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMTELLNPKTALFFLAVIPQFVKPATGHVFGQFLLLGTTSVVVNTLNAMLVATLAGFLGA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEVNLTNPKSIVFLAALFPQFIMPQQPQLM-QYIVLGVTTIVVDIIVMIGYATLAQRIAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSALIMASSLAFSVVKYAGAAYLIYLGLRVLLSKEALSSKEEASLAAAAPERQSRLFTQG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR-----G 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDGERPLGRPLTLVLRGFLVNASNPKAVIFMLAVLPQFIDPHQPLLAQYLIMGGTMIVVD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLQIGLALQIAIVAAGVGALLATSALAFSLIKWFGVAYLVYLAVRQWQAP-----PQALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFLVAAVVLALLPGPGLMYILARSLGGGR-----WAGIQSALGTGAGGMVHVLASAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIVMAGYTGLAARVLRVLRSPRQQKLVNRTFASLFVGAAGLLATVRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQSRRHLFQ-----RAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                  GB:U00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 228; DB 2;
Pred. No. 2.6e-14;
substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
  NID:g1788089;
in MG1655
                                                                                                                                                                                              Perna, N.T.; Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
                                                                                                                                                                                                                                   #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                    PIDN:AAC74868.1; PID:g17880
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                                                                                                                                                                                            V.; Riley,
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A; Experimental

source:

strain K-12,

C;Superfamily: hypothetical protein b1798

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A;Authors: Foolger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Togato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aththors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: F69975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dihydrodipicolinate reductase homolog yrhP - Bacillus subtilis C; Species: Bacillus subtilis
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                                             Qy
                                                                                                            В
                                                                                                                                                                                                             Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-210 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: F69975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: Z99117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Genetics:
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 RIALWIKGPKQM-KALNKIFGSLFMLVGALLAS
     122
                                                   114 AVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 FQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLAQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AWAGVATLIKTTPILFNIVRYLGAFYLLYLGSKILYAT----LKGKNSEAKSDEPQYGAI 116
                                                                                                                                                          63 LFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDL-----KSLASTQSR--RHLFQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 GWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLK---SLASTQSRRH--L 110
                                                                                                                                                                                                                  σ
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                                                                                                                                                                                                                                                                8 AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR-----GVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LNYW-TYLVGAIFIVLVPGPNTLFVLKNSVSSGMKGGYLAACGVF-----IGDAVLMFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKRALILSLTNPKAILFYVSFFVQFIDVNAPHTGISFFILAATLELVSFCYLSFLIISGA 176
     GSLSNILNPKTVLVYVTIMPQFINLNGNINQQLIILASILTLLAVLWFLFLVYIIDYAKK 181
                                                                                                         VIAKSVILETTIKYLGAAYLIYLGVKSFFAKSMFSLDDMQSQAKNMASSPKRYYKTSFMQ
                                                                                                                                                                                                             AYIPIAAMMVIIPGADTMLVMKNTLRYG-PKAGRYNILGLATGLSF---WTVIAILGLSV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                               18.4%;
27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; GB:AL009126;
168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 195.5; DB 2
Pred. No. 2.7e-11;
                                                                                                                                                                                                                                                                                                                                            Score 195; DB 2
Pred. No. 3e-11;
                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g2634966; PIDN:CAB14652.1; PID:g2635156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                                                                                                                                       Length 210;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 212;
                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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                                                                                                                                                                                                                                                                                                                    6,
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Query Match
Best Local Similarity
Matches 57; Conser
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hypothetical protein BH0429 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000 C;Accession: E83703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337 A;Accession: G83082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: G83082
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
A;Cross-references: GB:AP001508; GB:BA0000004; NID:g10172890; PIDN:BAB04148.1; GSPDB:GA;Experimental source: strain C-125
                                                     A; Molecule type: DNA
A; Residues: 1-207 <STO>
                                                                                                                                   A; Reference number: A; Accession: E83703
                                                                                                                                                                  A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A; Reference number: A83650; MUID: 20263314
                                                                                                                                                                                                                     R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: PA4507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004864; GB:AE004091; NID:g9950740; PIDN:AAG07895.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein PA4507 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAQRLQQWGFGGLLIGFGVRLALLR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPKALLFCSVLLPQFVSPEAGSLAVQFAALGTVLVLVGLAFDCAYALAGGRLGRWLASRP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLAQRIALWIKG-P 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPWTFDLVRLLGAVYLAWLGLQMLRGGGLALPTSDAGSAPVVPHADRRALLRGLLTNLL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSVIAFEVLKWAGAAYLIWLGIQQWRAAG-AIDLKSLAST----QSRRHLFQRAVFVNLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFLIALAVVYLVPGPDMLLLFQTGARQGRRAALVTALGLALARACHVLMAA-TGLALLFR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYC--WASDRTGDSYCAGWRGVGTLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMKNSKFQKVFQKITG - - IILVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 193; DB 2;
Pred. No. 4.6e-11;
11; Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106;
                                                                                                                                                                                                                                              Sasaki, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 210;
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                                                                                                                                                                                                                                              Masui, N.; Fuji, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Conservative

18.1%; Score 192.5; 26.3%; Pred. No. 5e-tive 50; Mismatches

5e-11; DB 2;

Length 207; Indels

87;

23;

Gaps

6

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conserved hypothetical protein VCA0355 [imported] - Vibrio cholerae (group Ol strain N: C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C;Accession: C82471
R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio A;Reference number A82035; MUID:20406833
A;Accession: G82200
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                 Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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A; Title: DNA Sequence of both chromosomes A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                   C82471
                                                                                                                                                                                                                                                                                  Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: VC1421
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-212 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGW--- 57
                                                                                                                                                                                                                                                                                LSSAKNLLKNASFMRWMEGTTGVVLVALGIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATFSAIGISAILAQSAELFQIVKMVGAAYLIWLGISSLRSLMKTGQGIEVASLAHAQFRL 113
                                                                                                                                                                                                                                                                                                                   AQRIALWIKGPKQMKALNKIFGSLFMLVGALL
                                                                                                                                                                                                                                                                                                                                                         TRSLREGFLSNVLNPKTAVFYLAFLPQFINPDYSPLAQSLLMALIHFAIAMVWQCGLAGA 173
                                                                                                                                                                                                                                                                                                                                                                                            HLFQRAVFV-NLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVIQNFEAFFIAITILTLTPGLDTALVIRNTSRAGFADG---C---TTSLGICFGLFVH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRIA-LWIKGPKQMKALNKIFGSLFMLVGALLASARH 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYATLA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRA----AGAIDLKSLASTQSRR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKVGQLLMRSSFIKNQMHRIKGGLLALIGLQVAFSKN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYKKGIIMNVLNPKVSLFFLALLPQFVNSGAGSAPWQMLLLGVVFLIQAFIIFSLVSWFA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITAAVVGISALIYQSALAFTVVKYAGAAYLLYLAWKAFQEKGEGLSIDKQ---TTLAYGA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAG---AIDLKSLASTQSRRH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDLTSLLSFLGVAVLLTLMPGPDILFVLAQSMSQNRQAGIV-----TALGLCTGLLVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.9%; Score 190; DB 2; 27.4%; Pred. No. 8.9e-11; tive 35; Mismatches 99
                of
                                                                                                                                                                                                                                                                              205
                                                                                                                                                                                                                                                                                                                     199
                the cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 212;
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              pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
            Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A; Gene: VCA0355
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A;Status: prelimina
                                                                                                                                                                                                                                                                                              Matches
              172
                                                      113
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A;Status, Francis DNA
A;Molecule type; DNA
A;Residues: 1-207 <STO>
A;Cross references: GB;AE004786; GB;AE004091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Gene: PA3665
C:Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337
A;Accession: D83187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA3665 [imported] - Pseudomonas aeruginosa
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A; Residues: 1-208 <HEI>
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Best Local Similarity 29.3%;
Matches 63; Conservative 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 LAQRIALWIKGPKQMKALNKIFGSLFMLVGALLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 KNVFVQGVIVSVLNPKVALFFLSFLPQFIDTSSGSASMQLLWLGLLFSVLVTMCNILYAS
                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 57; Conserva
ALWIKGPKQMKALNKIFGSLFMLVG-ALLASARHA
                                                RQEFLVAAGNPKAILIFTAFLPQFVDPGQPLGAQFAQLGAAFLLLEWLAIALYSYAGLHL
                                                                                              QRAVEVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLAQRI 171
                                                                                                                                                                                                                                                                                                WFAYLLTSIILTLSPGSGAINTMTTSLNHGYP----AGGVYCWASDRTGDSYCAGW----
                                                                                                                                              ASGLALVLHTSAWLFLAIKLLGAAYLLWLAVQLWRT----DAQPLANEASPARPSLWRLG
                                                                                                                                                                                            -RGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRR-----HLF 111
                                                                                                                                                                                                                                               WALFVPACFALNLAPGPNNLLSLNNAARHGFATASLAGGGRLLA-----FAGMLALA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGSWVFSRPNSQRYSRGLEGVSGVL--LIG--LAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYAT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTLAASLGLSAIILSSAVAFSAVKWLGAAYLVYLGVQSLLSMWR--GGSTLKVSESVESD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --CAGWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQ----QWRAAGAIDLKSLASTQSR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDLNSLLLFIVACLAINMIPGPDVIYIVSNTMKGKLVTGFKAAMGL-----GVGYFV 52
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                     17.0%;
26.5%;
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Pred. No. 6.9e-10;
4; Mismatches 97
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Pred. No. 2.1e-10;
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Larbig,
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K.; L
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A;Cross-references: GB:AE004079; GB:AE003849; NID:g9107960; PIDN:AAF85515.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, Bueno, M.R.P.; Camargo, A.A.; Ferreira, A.J.S. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri, D.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid transporter xF2730 [imported] - Xylella fastidiosa (strain 9a5c) C:Species: Xylella fastidiosa C:Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004889; GB:AE004091; NID:g9951014; PIDN:AAG08143.1; GSPDB:GN00: A;Experimental source: strain PAO1 C:Genetics: A;Gene: PA4757 C;Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-213 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The genome sequence of the plant pathogen A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see referenc A;Accession: C82523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: C82523
R;anonymous, The Xylella fastidiosa
Nature 406, 151-157, 2000
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C82523
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83051
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicladman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lari, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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A; Residues: 1-216 <STO>
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Best Local S
Matches 60
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; Pred. No. 7.2e-10; 
41; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consortium of the Organization for
                                                                                                                                                                                                                                                                                                                                                                                                                   reference number
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, A.; Larbig,
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K.; Lim,
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                                                             RESULT
C82139
        conserved hypothetical protein
C; Species: Vibrio cholerae
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179

VRLAAWFRRRQRLAAGATSGVGALFVGFGVKLATA

213

VC1939

[imported] - Vibrio

cholerae

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                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-216 < KWO>
                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: C55580
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Structure and regulation of the carAB A; Reference number: A55580; MUID:94222830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 176, 2532-2542, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pseudomonas aeruginosa
C;Date: 25-Aug-1995 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Kwon, D.H.; Lu, C.D.; Walthall, D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein (carA 3' region) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 YLLTSIILTLSPGSGAINTMTTSLNHGYPAG------GVYCWASDRTGDSYCAGWRG
                                                                                                        ALGVASLLKAEPMLFIGLKYLGAAYLFYLGVGMLRGAWR-KLRNPEATAGQAEQVDVHQR 119
                                                                                                                                         WRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSR-----RHL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMKALNKIFGSLFMLVGALLASAR 203
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                                     FRQALLLSLSNPKAILFFISFFIQFVDPGYAYPGL-SFLVLAVILELVSALYLSFLIFTG
                                                                      FQRAVFVNLTNPKSIVFLAALFPQFIMP--QQPQLMQYIVLGVTTIVVDIIVMIGYATLA 168
                                                                                                                                                                              DEW-TYVLGVVEVILLPGPNSLEVLATSAQRGVATGYRAACGVE-----LGDAVLMLLS 60
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25.0%;
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Pred. No. 1.1e-09;
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Pred. No. 1.1e-09;
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Silv
A.L.
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000 C;Accession: C82139 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: C82139 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-206 <HEI>A;Cross-references: GB:AE004269; GB:AE003852; NID:99656466; PIDN:AAF95087.1; GSPDB:GN001 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
Search completed: May Job time: 342 sec
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A; Gene: VC1939
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                                                                                                                                                       173 KGLKRLLSQAHHVRLLNRIAGSLMAGVGIWL 203
                                                                                                                                                                                                                                                                                                                                 109 HLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLA 168
                                                                                                                                                                                                 169 QRIALWIKGPKQMKALNKIFGSLFMLVGALL 199
                                                                                                                                                                                                                                                                              113 GLLVQGFVTAIANPKGWAFMVSLLPPFIDQSLSLAPQLTVLVAIILLSEFISMSLYATGG 172
                                                                                                                                                                                                                                                                                                                                                                                              69 IA-----FEVLKWAGAAYLIWLGIQQWRAAG--AIDLKSLASTQ-SRR 108
:| | :| ||:||:||:||:| ||::: :| |
53 VAVSAVVGIAAVMLRYPDIFTLFKIVGASYLVYLGVQMWRSRGKLAINIEQENTYQGSDW 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 FIPTFFFVSITPGMNMTLALTLGMSVGY------RRT----LWMMVGELLGVAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 YLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGYGTLFSRSV 68
                            6, 2001, 14:40:01
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
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P76249 escherichia
O05406 bacillus su
P38102 pseudomonas
P74343 synechocyst
P75693 escherichia
P38101 escherichia
P37005 pseudomonas
P11667 escherichia
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P77327
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P7
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                4 sargocentro
9 vibrio para
5 bacillus su
6 homo sapien
9 escherichia
7 kluyveromyc
5 thermoprote
6 mycobacteri
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                                                                                                                                                                                                                                                                                                                                                          0 salmonella
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0 haemophilus
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DR DR DR DR DR DR FT

EMBL; M87049; AAA67620.1; ALT\_FRAME.
EMBL; AE000458; AAC76827.1; ALT\_FRAME.
PIR; S30714; S30714.
EcoGene: EG11469; rhtB.
InterPro; IPR001123; -.
Pfam; PF01810; LysE; 1.

Transport;

Transmembrane.
5 25

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                                                                    "A 460-kb DNA sequence of the Escherichia coli K-12 corresponding to the 40.1-50.0 min region on the lin DNA Res 3:379-392(1996).

-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN -- I- SUBLEARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               P76249; 007971; 007969;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
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Mau B., Shao Y.;
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STRAIN=R12 / MG1655;
STRAINE=97426617; PubMed=9278503;
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RESULT 3
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                            Duesterhoeft A., Ehrlich S.D.;

"Sequence of the Bacillus subtilis genome region the lev operon reveals two new extracytoplasmic followerse sigma factors Sigv and Sigz.";

Microbiology 143:2939-2943(1997).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTE-
-!- SIMILARITY: BELONGS TO THE RHT FAMILY.
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                                                                                          Sorokin A., Bolotin A., Purnelle Duesterhoeft A., Ehrlich S.D.;
                                                                                                                                                    Kunst F., Ogasawara N.,
Submitted (NOV-1997) to
                                                                                                                                                                Kunst F.,
                                                                                                                                                                           STRAIN-168;
                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                  YRHP_BACSU 005406;
                                                                                                             MEDLINE=97453479; PubMed=9308178;
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EMBL; U93874; AAB80873.1; -.
SubtLList; BG12304; yrhP.
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-94222830; PubMed-8169201;
KWON D.-H., Lu C.-D., Walthall D.A., Brown T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PA4757.
                   MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                   "Structure and regulation of the carAB operon in aeruginosa and Pseudomonas stutzeri: no untransla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas.
NCBI_TaxID=287;
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Abdelal A.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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PROTEIN PA4757.
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sequence of Pseudomonas aeruginosa PAO1,
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Okumura S., Shimer.
Yamada M., Yasuda M., Ya
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Nature 406:959-964(2000).
                                                 MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Naka
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; TRANSMEM 12 3
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                                                                                                                                                                                                                                      Synechocystis
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUL-1998 (Rel. 3
HYPOTHETICAL 24.8 F
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
    Duncan M., Allen
Federspiel N., Hy
                                                   SEQUENCE FROM N.A.
                                                                                                                                                         Gregor J., Davis N.W.,
                                                                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Per
Riley M., Collado-Vides J., Glasner J.D., Rode
                                                                                                                                                                                                                                                                                                                                          Bacteria; P.
Escherichia
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TRANSMEM 9 2:
TRANSMEM 47 6:
TRANSMEM 74 9.
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                                                                                                                                       B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: INTEGRAL SIMILARITY: BELONGS TO THE RHT
                                                                                        complete genome sequence nce 277:1453-1474(1997).
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53; Conservative
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67 P
94 P
170 P
22041 MW;
    Araujo R.,
R., Kalman
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PROTEIN IN BETT-PRPR INTERGENIC
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Pred. No. 6.9e-07
1; Mismatches 9
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S., Komp
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A.M., Chung
C., Kurdi O.
                                                                                                                                                         Goeden
                                                                                                                                                  Perna N.T., Burland V ode C.K., Mayhew G.F., eden M.A., Rose D.J.,
                                                                                                             coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91;
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  Davis
ew H.,
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                SEQUENCE FROM N.A
                                                                                                                            Escherichia coli
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                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-K12;
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                                                                                                                                               Non-ribosomal proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

'!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

'!- SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                                translational apparatus,
                                                                                                   erichia coli.";
Nierhaus K.H. (eds.);
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                                                                                                                                                                                                                                                                                                       Proteobacteria;
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85 109
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223 LRLINGSVIOR -> YA (IN REF. 2)
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PROTEIN IN SRMB-UNG INTERGENIC
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                                                                                                                                                                                                                                                                                                     gamma
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                                                                              pp.185-195,
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                                                                                                                                               assembly
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                                                                                Plenum Press
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RESULT 8
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TRANSMEM 47 67
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TRANSMEM 142 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rudd K.E.;
Unpublished observations (AUG-1994).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H. Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K. Masuda S., Miki T., Mizobuchi K., Mori H., Motomura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                             KGPKOMKALNKIFGSLFMLVGALL 199
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                                                                                                                                                            CAGISFSLAVIDPAAVHLLSWAGAAYIVWLA--
                                                                                                                                                                                   GVGTLFSRSVI----AFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAV
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nce 277:1453-1474(1997).
                                                   LAGHLFQRLFRQYGRQLNIVLALL
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D64044; -; NOT_ANNOTATED_CDS.
AE000344; AAC75631.1; -.
                                                                                                        ALQFVNVKIILYGVTALSTFVLP-QTQALSWVV-GVSV----LLAMIG--TFGN--VCWA
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ne; EG12445; yfik.
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                                                                                                                                                                                                                                                                             Score 126; DB 1
Pred. No. 6e-05;
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STRAIN=K12 / MG1655;

MEDLINE=92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burla
"Analysis of the Escherichia coli ge
from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
[2]
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01-AUG-1992
15-JUL-1998
15-JUL-1999
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                                                              EMBL;
                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                This
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FEBS Lett. 452:228-232(1999).
-i- FUNCTION: CONDUCTS THE EFFLUX OF THREONINE.
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                       EcoGene; EG11468; rhtC InterPro; IPR001123; -
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Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R
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             Pfam; PF01810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87115164; PubMed=3027506;
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                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN SIMILARITY: BELONGS TO THE RHT FAMILY. CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAINTRODUCED IN POSITION 80 TO PRODUCE THIS ORF.
                                                                                                                                                                                                                        CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 47 AND 73.
                                                 ## M87049; AAA67619.1; ALT_FRAME.
## AE000458; AAC76826.1; ALT_FRAME.
## M30198; -; NOT_ANNOTATED_CDS.
## S30713; S30713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o N., Nakayama K., Nakayama H.
recQ gene of Escherichia coli
ence for SOS regulation.",
Gen. Genet. 205:298-304(1986)
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oli genome: DNA sequence
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                                                                                                                              http://www.isb-sib.ch/announce/
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087005;
15-JUL-1999
15-JUL-1999
01-OCT-2000
CHEMOTACTIC
                                                                                                               Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:595-964 (2000).

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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                                                                     ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
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  U79580;
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                                   (See http://www.isb-sib.ch/announce/
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01-OCT-1996
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                                                                                                           MEDLINE=89313302: PubMed=2546007;
Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
Identification, molecular cloning and sequence analysis of a gene cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3 phosphoglycerate kinase and a putative second glyceraldehyde 3-phosphate dehydrogenase of Escherichia coli.";
Mol. Microbiol 3:723-732(1989).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                  modified
                                                           between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                    This
                                                                                                                                                                                                                              SEQUENCE OF 15-211 FROM STRAIN=K12 / CS520;
                                                                                                                                                                                                                                                                  "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                "The
                                                                                                                                                                                                                                                                                          Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAINE=97426617; PubMed=9278503;
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                                                                       SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
39; Conser
         non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria;
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PROTEIN IN SBM-FBA INTERGENIC
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ayhew G.F.
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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
14YPOTHETICAL 21.5 F
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                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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              Hypothetical
                       InterPro; IPR001123; -.
Pfam; PF01810; LysE; 1.
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                                                                                                                                                                                                           Swift S., Ka Williams P.,
                                                                                                                                                                                                                                    STRAIN=NCIMB 1102;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=645;
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
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                                               EMBL; U65741; AAB70019.1; ALT_INIT.
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                                                                                                                                                                       SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                               ft S., Karlyshev A.V., Fish L., Durant E.L., Winson M.K., liams P., Macintyre S., Stewart G.S.A.B.; nitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE)
                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Last annotation update)
PROTEIN IN ASAR-CDPD INTERGENIC REGION
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P77327;
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SEQUENCE
                                                                                                                                                                                           Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: PERMEASE THAT IS INVOLVED IN THE TRANSPORT ACROSS THE CYTOPLASMIC MEMBRANE OF PROLINE.

-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIR-12 / MG1655;
STRAIR-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROY
                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
                                   EMBL; AE000146; AAC73505.1; EMBL; U82664; AAB40158.1;
                                                                                                                                                                                                                                                                                        STRAIN-K12;
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                                                                          an email to license@isb-sib.ch).
                                                                                                                                         the Swiss Institute of Bioinformatics
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EMBL; U82664; AAB EcoGene; EG13609;

InterPro;

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01-NOV-1997
30-MAY-2000
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the Eurc
                                                         This
                                                                        Liao M.K., Gort S., Maloy S.;
"A cryptic proline permease in Salmonella typhimurium.";
microbiology 143:2903-2911(1997).
-i- FUNCTION: PERMEASE THAT IS INVOLVED IN THE TRANSPORT AND CYTOPLASMIC MEMBRANE OF PROLINE.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER-
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercipean Bioinformatics Institute. There are no restr
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50; Conservative
           non-profit institutions as long and this statement is not removed.
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         Vrljic M., Sahm H., Eggeling L.;
"A new type of transporter with a new type of lysine export from Corynebacterium glutamicum. Microbiol. 22:815-826(1996).
                                                                                                                                                                                                                                                                                                                          LYSE_CORGL STANDARD; PRT; 236 AA. P94633; P5-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) LYSINE EXPORTER PROTEIN.
                                                                                                       MEDLINE=97126810; PubMed=8971704;
                                                                                                                           STRAIN=R127
                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                Corynebacterium glutamicum (Brevibacterium flavum).
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STRIN-RD / KW20 / ATCC 51907;

REDILINE-9535630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., McKenney K., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fehrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                     "Whole-genome random sequencing and assembly of Haemophilus influenzae {\tt Rd} .";
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                                               GLLVNLSNAKVVVYFSSVM-SLVLVNITEMWQ-IILAFAVIVVETFCYFYVISLIFSRNI
                                                                         AVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVD-----IIVMIGYATL
                                                                                                                                                                                                                                                                                                             PF01810;
                                                                                                                                                    l Similarity 21.1 32; Conservative
                                                                                                                                                                                                                                                                                                                           IPR001123;
                                                                                                                                                                                                              1 protein;
42 62
66 86
126 14
147 16
189 20
210 AA;
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                                                                                                                                                                                                                                                                                                            LysE; 1.
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86
146
167
209
                                                                                                                                                               8.2%;
                                                                                                                                                                                                                    23636
                                                                                                                                                                                                                                                                               Transmembrane.
2 POTENTIAL.
                                                                                                                                                                                                                    MW;
                                                                                                                                                  36; Mismatches
                                                                                                                                                              Score 87; DB 1; Length 210; Pred. No. 0.29;
                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                    254D159014845473 CRC64;
200
                                                                                                                                                    66;
                                                                                                                                                    Indels
                                                                                                                                                    18;
                                                                                                                                                   Gaps
                                                                                                                                                   5,
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Search completed: Job time: 191 sec мау 6, 2001, 14:41:20

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
     SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plage:*
10: sp_plage:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                              374700 seqs, 117207915 residues
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Gapop 10.0 , Gapext 0.5
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1061
1 MTLEWWFAYLLTSIILTLSP......KIFGSLFMLVGALLASARHA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May 6, 2001, 14:36:44 ; Search time 35.64 Seconds (without alignments) 674.176 Million cell updates/sec
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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                                                                                                                                                                                                                                                                                                                                                                                                                   374700
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

206 2	201010	**********************
	CALONO	Q916n6 salmonella
	Q9KVK7	
	Q9RSX2	
	Q9R6F8	
	Q9KFP9	
	Q9R6J5	
	Q9KS40	_
	Q9КМJ3	
	Q9XBR8	Q9xbr8 zymomonas m
	Q9RMX0	Ξ.
	Q9P9Z0	Q9p9z0 xylella fas
206 2	Q9KQQ9	
153 2	Q53934	Q53934 shewanella
208 2	Q9K775	Q9k775 bacillus ha
204 2	Q9KLA0	Q9kla0 vibrio chol
211 2	Q9X8L9	Q9x819 streptomyce
212 2	Q9L6H7	Q916h7 brucella me
206 2	Q9L6N7	~
209 2	Q9KKV0	Q9kkv0 vibrio chol
	205 205 207 207 207 207 207 207 207 207 207 207	000000000000000000000000000000000000000

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7.5	7.5	7.5	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.7	7.8	7.8	7.9		8.0				9.6		11.9	12.0
473	276	517	424	649	557	557	551	495	322	801	272	266	581	499	199	297	190	517	484	204	366	4588	210	212	222
N	N	N	2	N	N	N	10	N	ω	2	1	2	w	Ν	N	2	2	ω	2	N	N	G	N	N	Ν
005182	Q9KT31	050585	Q9K652	Q9KE20	Q9S6V2	Q56175	Q9XGP5	P73227	Q9T6Q7	Q9ZNG6	Q9V1K8	086829	014035	Q9RDF5	Q9KX85	Q9KBL4	068026	Q9Y860	Q9KX27	Q9KRD0	Q9K9S9	Q94709	Q9K8S1	Q9RIFO	Q9KVF5
005182 bacillus me	Q9kt31 vibrio chol	050585 arthrobacte	Q9k652 bacillus ha		Q9s6v2 streptomyce	Q56175 streptomyce	Q9xgp5 oryza sativ		Q9t6q7 trachemys s		Q9v1k8 pyrococcus	086829 streptomyce	014035 schizosacch	Q9rdf5 streptomyce	Q9kx85 staphylococ	Q9kbl4 bacillus ha	068026 rhodobacter	Q9y860 emericella		Q9krd0 vibrio chol	-			Q9rif0 yersinia en	

## ALIGNMENTS

Qy	Дb	Qy	ДĎ	Qy	<b>9</b> H	n	SQ	DR	R X	2 2	R P	RN	RL	RY.	RA	RC	RР	RN	X <sub>O</sub>	ဂ္ဂ	ဂ္ဂ	SO	GN	DE	ΤΩ	ΡŢ	DT	AC	ΙD	RES O91
115 VFVNLTNPKSIVELAALEPQEIMPQOPQLMQYIVLGVTTIVVDIIVMIGYATLAQRIALM 174 :{	56 LVGVGLGTLFSRSLLAFEILKWAGAAYLIWLGIQQWRAAGAIDLHTLAQTQSRGRLFKRA 115	59GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTOSRRHLFQRA 114	1 MTFEWWFAYLLTSTLLSLSPGSGAINTMTTSINHGY-RGAVASIAGLQTGLGIHIV 55	1 MTLEWMFAYLLTSIILTLSSFGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWR 58	Similarity 78.2%: Pred. No. 5.3e^65; 5; Conservative 15; Mismatches 20; Indels		SEQUENCE 206 AA; 22322 MW; E089B357D30750F2 CRC64;	33324; AAF33432.1;	Waterston K.; Submitted (FRB-2000) to the EMBL/GenBank/DDBJ databases.	STRAIN-SGSC1412	SEQUENCE FROM N.A.			"The Salmonella typhimurium Genome Sequencing Project.";	Washu;	STRAIN=SGSC1412;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=99287;		Bacteria; Profeobacteria; gamma subdivision; Enterobacteriaceae;	Salmonella typhimurium LT2.	RTHB.	Z	(TrEMBLrel. 15, Last	(TrEMBLrel, 15,	01-OCT-2000 (TremBLrel. 15, Created)		Q9L6N6 PRELIMINARY; PRT; 206 AA.	RESULT 1

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RESULT
Q9RSX2
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AC Q9
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Best Local :
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01-ОСТ-2000 (ТІЕМВЬІЖЕІ. 15, СК

01-ОСТ-2000 (ТІЕМВЬІЖЕІ. 15, Б.

01-ОСТ-2000 (ТІЕМВЬІЖЕІ. 15, Б.

НУРОТНЕТІСАЬ РЯОТЕІN VC0136.
                                                                                                                                                                                                                       Q9RSX2
O9RSX2;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-JUN-2000 (TrEMBLrel. 1
CONSERVED HYPOTHETICAL PF
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TIGR; VCC
SEQUENCE
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STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDILNE=20406833; PubMed=10952301;

MEDILNE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                              Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
EMBL; AE004104; AAF93313.1;
TIGR; VC0136;
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89; Conserv
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Pred. No. 3.3e
14; Mismatches
                                                                                                                group;
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                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-MARF301001;
SUZUKİ K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
SUZUKİ K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
SUZUKİ K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
Novel structural difference between nopaline- and octopine- type
gene:construction of genetic and physical map and sequencing of
trb/traI and rep gene clusters of a new Ti plasmid pTi-SAKUKA.";
Biochim. Biophys. Acta 1396:1-7(1998).
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INTERPRO; IPRO01133; -.
PFAM; PFO1810; LYSE; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
SEQUENCE 241 AA; 25161 MW; A4017ABFEDB60374 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K., Katoh A., Yoshida K.; Katoh A., Iwata K., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MAFF301001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pTi-SAKURA.
Batteria: Proteobacteria: alpha subdivision; Rhizobiaceae
Rhizobiaceae: Agrobacterium.
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Science 286:1571-1577(1999).
Science 286:02037; AAF11548.1;
TIGR; DR1999; -...
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    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium tumefaciens
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54; Conservative
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Pred. No. 1.1e-12
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EMBL; AP00
SEQUENCE
          SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Taka
Submitted (MAR-2000) to the
EMBL; AP001508; BAB04148.1;
                                                                            Bacillus halodurans:
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID-86665;
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AB016280; BAA87726.1; -.
PRO; IPR001123; -.
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f pTi-SAKURA (III): Characteristics
Ser. 39:185-186(1998).
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15,
                                  Takaki Y.;
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Pred. No. 6.7e
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9FED148C8E8DD3F0 CRC64;
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No. 6.7e-10;
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Best Local S
Matches 57
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SEQUENCE FROM N.A.
STRAIN-MAFF301001;
Uraji M., Suzuki K., O
Uraji M., Structure of F
                                         Nucleic
[6]
                                                                                                                                                                                                                      Ohta N., "Genome
STRAIN-MAFF301001;
                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K. "Novel structural difference between nopaline- and octopine- t gene:construction of genetic and physical map and sequencing of trb/tral and rep gene clusters of a new Ti plasmid pTi-SAKURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MAFF301001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suzuki K., Hattori
Katoh A., Yoshida F
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Rhizobiaceae; Agrobacteri
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01-MAY-2000
                                                                                                                                                                                                                                                                    STRAIN-MAFF301001;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                              Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., 1
"Genome structure of pTi-SAKURA(I): Strategy for DNA
Japanese cherry-Ti plasmid.";
Nucleic Acids Symp. Ser. 37:159-160(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence Gene 242:331-336(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYKKGIIMNVLNPKVSLFFLALLPQFVNSGAGSAPWQMLLLGVVFLIQAFIIFSLVSWFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAG---AIDLKSLASTQSRRH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDLTSLLSFLGVAVLLTLMPGPDILFVLAQSMSQNRQAGIV-----TALGLCTGLLVH
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57; Conserv
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                                                                                                                                                                                                                                           Suzuki K.,
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Agrobacterium.
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                                                                                                                                                                                               Hattori Y., Uraji M., Katoh A., Yof pTi-SAKURA (III): Characteristics Ser. 39:185-186(1998).
                                                              Ohta N., Hattori Y., Katoh A., Yo pTi-SAKURA (IV): Characteristics Ser. 39:187-188(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.1%;
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Last annotation updat
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Pred. No. 1.2e-09;
0; Mismatches 87;
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                                                                                                          Yoshida K.;
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ics of T-DNA.";
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A sequencing
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of
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Q9KS40;
Q1-OCT-2000 (TrEMBLrel. 15, C)
Q1-OCT-2000 (TrEMBLrel. 15, L)
Q1-OCT-2000 (TREMBLrel. 15, L)
PHYPOTHETICAL PROTEIN VC1421.
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Best Local
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayyam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
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EMBL; AB016260; BAA87689.1; -.
INTERPRO; IPR001123; -.
INTERPRO; IPR001123; -.
                                                                                                                                                                                                                                                                                                                              EMBL; AE004221; AAF94578.1; TIGR; VC1421; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence of both chromosomes cholerae.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVMIGYATLAQRIALWIKGPKQMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STQSRRHLFQRAVFVNLTNPKSIVFLAALFPQFI----MPQQPQLMQYIVLGVTTIVVDI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEISTLLAFAAAFFVFAASPGPDNMTIVARTISNGAASGIAY----
                                                                             MVIQNFEAFFIAITILTLTPGLDTALVIRNTSRAGFADG---C---TTSLGICFGLFVH
                                                                                                                            MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERRGLLAVFATGVALNLGNPKMPLFYVALLPNVVGSSLTPGHLAALAAVILAVEAVVIG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria; gamma
RGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRA----AGAIDLKSLASTQSRR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229
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                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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27.4%;
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Pred.
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Pred. No. 1.4e-09;
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No. 2
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RESULT
Q9XBR8
ID Q9
AC Q9
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DT 01
DT 01
DT 01
DT 01
CH HY
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CN ZM
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Best Local
                                      Q9XBR8 PRELIMINARY;
Q9XBR8;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-JUN-2000 (TrEMBLrel. 1
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Q9KMJ3;
Q1-OCT-2000 (TrEMBLrel. 15, Creat
01-OCT-2000 (TrEMBLrel. 15, Last
01-OCT-2000 (TrEMBLrel. 15, Last
uvpothetical protein VCA0355.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson
              HYPOTHETICAL ZM100RF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004372; AAF96263.1; TIGR; VCA0355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholerae.
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Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
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Zymomonas mobilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                  VGSWVFSRPNSQRYSRGLEGVSGVL-
                                                                                                                                                                                                                    KNVFVQGVIVSVLNPKVALFFLSFLPQFIDTSSGSASMQLLWLGLLFSVLVTMCNILYAS
                                                                                                                                                                                                                                               RHLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIVMIGYAT
                                                                                                                                                                                                                                                                            HTLAASLGLSAIILSSAVAFSAVKWLGAAYLVYLGVQSLLSMWR--GGSTLKVSESVESD
                                                                                                                                                                                                                                                                                                     ---CAGWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQ----QWRAAGAIDLKSLASTQSR 107
                                                                                                                                                                                                                                                                                                                                MDLNSLLLFIVACLAINMIPGPDVIYIVSNTMKGKLVTGFKAAMGL-----GVGYFV
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                                                                                                                                                                                          LAQRIALWIKGPKQMKALNKIFGSLFMLVGALLAS
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                         9 (TrEMBLrel. 12,
0 (TrEMBLrel. 14,
AL 17.5 KDA PROTEI
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                              PRELIMINARY;
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                            KDA PROTEIN.
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                                                                    Created)
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Pred.
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ey E.K., Peterson J.D., Umay
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                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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No. 4.7e-09
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RESULT
Q9RMX0
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Best Local
                                                                                                                                                                                                                                         Brown A.E., Jacksum....Brown A.E., Jacksum....Brown A.E., Jacksum.... the Submitted (NOV-1999) to the EMBL, AF188935, AAF13668.1, TNTERPRO; IPRO1123; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                               Okinaka R.T., Cloud K., Hampton O., Kumano S., Manter D., Martinez Y., Brown A.E., Jackson P.J.;
                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1392;
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                            Okinaka R.T., Cloud
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid
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113 RAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDII---VMIGYATLAQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
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                                                                                                             1 MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAG-GVYCWASDRTGD----SYCA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.W., Kang
he sequence
                           --IGIGVIISKSILLFNTLKWIGVAYLLYIGIKLLRSKKQSPAAIIKNNESTTWK--AFR 113
                                             GWRGVGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRA---AGAIDLKSLASTQSRRHLFQ 112
                                                                                   MDLNIWITVLLYGTIGVISPGPNWAVIIKNSL---YSRSLGVSTVAGIATGSLIHIVYCL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt GLGAVLRASELAYNLIKWSGAAYLCWLGINLLIHPRKNLVDNLDPSMPSATKALRQGF--}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LWIKGPKOMKALNKIFGSLFMLVGALLASAR 203
                                                                                                                                                                                                                                       РКО; IPROO1123; -.
PF01810; LysE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --FTNILNPKYGIFYYTFLPQF-MPSSSHLIQYAFL--LTFIHAMITILWFAILALATAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               htted (JUN-1999)
AF157493; AAD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               pxO2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteobacteria; alpha subdivision; Sphingomonas group;
                                                                                                                                                                                                                205
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.S.;
analysis
                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD42407.1;
                                                                                                                                                       17.3%; 29.5%;
                                                                                                                                                                                                                22900 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.4%;
30.1%;
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                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update;
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                       Score 184; DB 2
Pred. No. 7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 184.5; DB 2
Pred. No. 4.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                             6DC91EE968B524B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FE44A9639DA75A64 CRC64;
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                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                            Svensson
                                                                                                                                                                                                                                                                                                                        Hill K.K., Keim P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone of Zymomonas mobilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                            R.,
                                                                                                                                                                    2; Length 205
                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                          Indels
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Q9P9Z0
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Lemes M.J., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Macnado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Mancke C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Niyaki C.Y., Monteiro-Vitorello C.B.,
RA Monn D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Monto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A.,
RA da Silva M.A., Tat., Turuffi D. Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
"The Gromme Secondres of the Near tathorn Vicilia fatilities"."
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome sequence of the plant pathogen Xylella fastidiosa.", Nature 406:151-157(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMINO ACID TRANSPORTER. XF2730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF01810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE004079; AAF85515.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
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                                                                                                   73
                                                                                                                                                               60
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                                                                                            ISTVLKEYPSIYTGLQGIGAAYLLYIAYLSWPRQNASNQTPTASRSSYTGTFIQGVLINL 132
                                                                                                                                                   VGTLFSRSVIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNL 119
                                                                                                                                                                                                                                                                               YLLTSIILTLSPGSGAINTMTTSLNHGYPAG-----GVYCWASDRTGDSYCAGWRG
                                                                                                                                                                                                                   FILTVLMFSISPGPAMMFVLQQSQKNGVKTGLAAVLGTEIGVFIYV------ILTALG
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810; LysE;
213 AA; ;
                                                                                                                                                                                                                                                                                                                                               Conservative
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25.0%;
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                                                                                                                                                                                                                                                                                                                                               38;
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                                                                                                                                                                                                                                                                                                                                                                            Score 178.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E97242DD507C8065 CRC64;
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01-NOV-1996
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Q53934;
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TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-EL TOR N16961 / SEROTYPE 01; MEDLINE=20406833; PubMed=10952301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KQQ9;
                                                              Shewanella colwelliana (Alteromonas Bacteria; Proteobacteria; gamma subc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL
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                   NCBI_TaxID=23;
                                             Shewanella.
                                                                                                                                        MLGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVDIIVMIGYATLA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAGWRGVGTLFSRSV
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L PROTEIN VC1939.
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Last sequence
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Pred. No. 2.7e
35; Mismatches
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                                                                  subdivision;
                                                                                                                                                           sequence up
annotation
                                                                                          colwelliana)
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.7e-07;
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                                                                  Alteromonadaceae;
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Q9K775;
Q9K775;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DIHYDRODIFICOLINATE REDUCTASE.
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Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; X67020; CAA47413.1;
INTERPRO; IPRO01123;
PFAM; PF01810; LysE; 1.
SEQUENCE 153 AA; 16579 MW; A9F3167C965BB34F CRC64;
                                                                                                                                                                                                                                                                                                                                STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Tubmitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AP001519; BAB07214.1; -
SEQUENCE 208 AA; 23158 MW; CAD7A46D63B8E45
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus halodurans.
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                                                                                                                                                                                      VIAFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHLFQRAVFVNLTNPKSIVF
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                                                                                                                                LAALFPQFIMPQQPQL-MQYIVLGVTTIVVDIIV--MIGY--ATLAQRIALWIKGPKOMK 182
                                                               YMNIAATIIFIGLGLKLMTTQ
                                                                                    ALNKIFGSLFMLVGALLASAR
                                                                                                               YLTFLPQFVNYQSANISLQLCILGLIFIIMTAIIFSIFGYFSGTFRDRL---LKNSRFNE
                                                                                                                                                                 VVVFTIFKLAGAMYLFYLAYKALKHRKEEIRVNSEKTNDLKGLFLRGLIMNVLNPKVAIF 129
                                                                                                                                                                                                                  FMGSAIMLIIIPGPDLVFTITQGMTNGRKAGVITAMGLSLGNIVHTLAAVLGLSLIIQTS
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                                                                                                                                                                                                                                                                   Score 154.5; DB 2;
Pred. No. 2.8e-06;
4; Mismatches 100;
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Pred.
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No. 1.8e-06;
51
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Q9KLA0

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Search completed: May
Job time: 246 sec
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Best Local Similarity 27.4:
"~*~hes 46; Conservative
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCA0846.
Vibrio cholerae.
Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000).
EMBL; AE004412; AAF96744.1; -.
TIGR; VCA0846; -.
SEQUENCE 204 AA; 21719 MW; D09887299659FBBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           \ensuremath{^{\text{TDNA}}} sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=666;
                                                                                                 110 LFQRAVFVNLTNPKSIVFLAALFPQFIMPQQPQLMQYIVLGVTTIVVD 157
                                                                              115 ---EGLLISLLSPKIALFFIALFSQYVAVGS-DLTSKAAIVITPLVVD 158
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                                                                                                                                                                                                                                           1 MTLEWWFAYLLTSIILTLSPGSGAINTMTTSLNHGYPAGGVYCWASDRTGDSYCAG---- 56
                                                                                                                                                                                                               MTLTVWLSLFTICILGAMSPGPSLAMVAKHSLAGGRKNGFAAAWA-----HAFGIGVYAF 55
                                                                                                                                                                                                                                                                                            13.5%; 27.4%;
                 2001, 14:40:50
                                                                                                                                                                                                                                                                         5%; Score 143.5; DB 2;
4%; Pred. No. 2.6e-05;
27; Mismatches 74;
                                                                                                                                                                                                                                                                                                           Length 204;
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9b_est82:BF043998
gb_est92:AF09938
gb_est90:BF679835
gb_gss1:AF095402
gb_est44:AW290151
gb_est96:BG128211
gb_est96:BG12821
gb_est72:BE334024
gb_est72:AF34024
gb_est81:AF151505
gb_est18:AF34024101
gb_est818:BF4892242
gb_est88:BF4892242
gb_est87:AG525982
gb_est87:AG525982
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gb_est83:BF128485
gb_est39:AV651857
gb_est39:AV651904
gb_est39:AV651904
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gb_est11:AA735580
gb_est86:BF345786
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gb_est78:BE784988
gb_est88:BF526220
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Database length: 73081774
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gb_gss24:AZ601442
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length: 205
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AQ641276 RPCI93-DpnII-29E21.TJ
BE745367 601578883F1 NIH_MGC_9
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gb_est74:BE439347
gb_est89:BF612680
gb_est28:AL503330
gb_est73:BE412566
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Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ859250 473 bp DNA GSS 03-NOV-1999 nbeb0011L14r CUGI Rice BAC Library (ECORI) Oryza sativa genomic
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A BAC End Sequencing Framework to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.
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/note=west-be. Coll Datus
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/note=west-be. DBACINDigo; Site_1: EcoRI; Site_2: EcoRI;
/note=west-be. Coll Datus
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the hunid tropics and subtropics, rely
on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n-24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximatley 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99 9 8. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="nbeb0011L14r"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/tissue_type=""Leaf"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
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0 daa20a09.y1 NICHD 2
0 AL503330 Hordeum vu
6 MCG002.F11R990625 :
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Ratio:

227.00 4.633 92.453

Percent Identity:

86.792

Length:

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alignment_block:
US-09-466-935-2 x AQ859250/rev
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BG038404 BG038404.1 GI:12480989
EST:
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Washu Xenopus EST project, 1999
Unpublished (1999)
Other_ESTs: dg34h08 x1
Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                        Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus
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                                                                                                                                                                                                                                                                                            Seq primer: -40RP from Gibco
High quality sequence stop: 430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
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314 286 1810
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/note-"Vector: pBluescript SK-; Site_1: ECORT; Site_2: XhOI; cDNA was prepared from 2ug of poly A+ RNA (equal parts from stage 10.5 and stage 11.5 gastrulae). ECORI-XhOI cut cDNA was then ligated into UniZap-XR
                                                                                       /clone="XENOPUS_SOURCE_ID:xlnnga009p16"
/clone_lib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F'"
                                                                                                                                                                                               /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                    Location/Qualifiers
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SOURCE

ORGANISM

Xenopus

laevis

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alignment_block:
US-09-466-935-2 x BG038404
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                                                                                                                                            seq_documentation_block:
LOCUS BF614897
                                                                                                                                                                                                         seq_name: gb_est89:BF614897
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Percent Similarity:
                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                290 GAAACGAGGCAGCCGCAAAAAGCCGCCCGCGTCATCGGTGAGGCGATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TyrLeuLeuThrSerIleIleLeuThrLeuSerProGlySerGlyAlaIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPh 116
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                                                          dg18a02.yl Xenopus laevis gastrula non normalized Xenopus laevis cona clone XENOPUS_SOURCE_ID:Xlnnga005b04 5' similar to TR:Q9RSX2 CONSERVED HYPOTHETICAL PROTEIN. ;, mRNA sequence.
                  BF614897.1 GI:11787968
EST.
African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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a 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Stratagene) with EcoRI at the 5' end and XhoI at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and
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                                                                                                                                                                                                                  15 IleLeuThrLeuSerProGlySerGlyAlaIleAsnThrMetThrThrSe
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48 rgThrGlyAspSerTyrCys.......
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Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, M., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            below when ordering this clone: Source lab clone id - xlnnga005b04 Seq primer: -40RP from Gibco High quality sequence stop: 401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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1 (bases 1 to 428)
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/db_xref="taxon:8355"
/db_xref="taxon:8355"
/clone="xenopus_Source_ID:xlnnga005b04"
/clone="Xenopus laevis gastrula non normalized"
/clone_Ib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F/"
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCTGCAGGAGAATGGCGCGCTGAAGATCGATGAAACGAGGCAGCCGCAA
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AQ365906.2 GI:6585776
GSS.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ365906 562 bp DNA
nbxb0064N05f CUGI Rice BAC
nbxb0064N05f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
On Dec 15, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 400.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
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ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_gss12:AQ858095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-466-935-2 x AQ365906
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                           COMMENT
                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                    REFERENCE
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Percent Similarity:
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                                                                      AUTHORS
TITLE
                                                                                                                                                                                                             ORGANISM
                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTACCTGGTGTATCTGGGTGTG 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..........TGGCGCGGTTACTGGAACGCCCTCGGTCTGCA 438
                                                                                                                                                                                                                                                                                                                    AQ858095 769 bp DNA GSS 03-NOV-1999 nbeb0011L14f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0011L14f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Clemson University Genomics Institute
                                           Wing,R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                             Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                             GSS.
                                                                                                                                                            Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                           Contact: Wing RA
                                                                                                                                                                                                                                                                                 AQ858095.1 GI:6208552
                                                                                                                    (bases 1 to 769)
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2.534
54.630
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Percent Identity: 27.778
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ACCESSION

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alignment_block:
US-09-466-935-2 x AQ858095
                                                                                                                                                                     seq_name: gb_gss23:AZ576789
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                                                                                        seq_documentation_block:
LOCUS AZ576789
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                                                                                                                                                                                                                                  ACGGGTAT
01a12 Shot-gun genomic library of Rhizobium strain sp. NGR234 genomic clone 01a12, DNA sequence. a2576789
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100 Jordan Hall, C
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Fax: 864 656 4293
Email: rwing@clemson.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_nost="E. Coll Dalua"
/note="Wector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
we have constructed a BAC library from Oryza sativa.
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximatley 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

203 a 216 c 176 g 169 t 5 others
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3.500
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Gaps: 0
Percent Identity: 91.667
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                                                                ANU265 Rhizobium
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us-09-466-935-2.rst

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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="ANU265"
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ANU265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note "Vector: M13; derivative strain of NGR234 cured of
                                           Rhizobium sp. NGR234.
Rhizobium sp. NGR234
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
1 (bases 1 to 407)
                                                                                                                                                 Viprey V.V. Rosenthal, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome GenomeBiology.com 1 (6), 0014.1-0014.7 (2000)
Contact: Virginie Viprey
Laboratoire de Biologie Moleculaire des Plantes Superieures University of Geneva
1 Chemin de 1/ Imperatrice, Chambesy/Geneva 1292, Switzerland Fax: +44(0)1603450000
Fax: +44(0)1603450005
Email: virginie.viprey@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 CATGGACATGGTCTTCGTGCTGGCCAACGCGATAACCGGCGGACGCAGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CCGGCCTCGCCGCGCGCGCGCATCATGCCAGGCGGCGTGCTGCACACG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 .....CTCTATGCCGCG.....CTCGGCGTCACGTCGTCTTGCATCT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 SerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAlaValPh 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 eValAsnLeuThrAsnProLysSerIleValPheLeuAlaAlaLeuPheP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 laGly.....GlyValTyrCysTrpAlaSerAspArgThr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 gSerValIleAlaPheGluValLeuLysTrpAlaGlyAlaAlaTyrLeuI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ySerGlyAlaIleAsnThrMetThrThrSerLeuAsnHisGlyTyrProA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 GlyAspSerTyrCysAlaGlyTrpArgGlyValGlyThrLeuPheSerAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 leTrpLeuGlyIleGlnGlnTrpArgAlaAlaGlyAlaIleAspLeuLys 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GACGAGCCTGATGAANCCGAAGGCCTATCNCTTCATGTTCGCCGNCTACC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLeuSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GAGGCGGGGGGGAGGCTCTCGCGCTGGGCGAGCTTTCGACAGGGGGGCGCT
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Percent Identity: 28.148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137
    GI:11603030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-466-935-2 x AZ576789/rev
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1.394
59.259
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                                                                                                                                                                                                                                                                                                                                                                         Class: shotgun
    AZ576789.1
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                                                                ORGANISM
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AUTHORS
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JOURNAL
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VERSION
KEYWORDS
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 932)
S NIH-MGC http://mgc.nci.nih.gov/.
S NIH-MGC http://mgc.nci.nih.gov/.
Ontoublished (1999)
VI Oppublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausbergenih.gov
Tissue Procurement DCTP/DTP/PGazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9649 row: j column: 08
High quality sequence stop: 602.

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             BE784988 932 bp mRNA EST 20-OCT-2000 601478429F1 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:3881191
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193 CTCACACTCCCATGGTGGAGGAGACAGCAGCATGATGATGATGCCTATGA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27, hrMetThrThrSerLeuAsnHisGlyTyrProAlaGlyGlyValTyrCys 43
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Gaps: 14
Percent Identity: 24.034
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192 c 259
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BE784988.1 GI:10206186
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US-09-466-935-2 x BE784988
                                                                                                                                                                                seq_name: gb_est78:BE784988
                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                     seq_documentation_block:
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Ratio:
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133 roGln 134
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                                                                                          13 CGCAG
                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
COMMENT
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9

	/organ
hrLeuPheSerArgSerVallleAlaPhe.GluValLeuLysTrP ::::    :::     ::::    :::     ::::    :::     :::    :::	/db_xrv /clone- /clone- /lab_h /lab_h /ncte= Site_2 Site_3
93 aGlyAlaileAspLeuLysSerLeuAlaSerThrGlnSerArgArgHisL 110	BASE COUNT 148 a 19 ORIGIN
110 eupheGlnargalaValPhe.ValAsnLeuThrAsnProLysSerIleVa 126 :::        ::: :::    ::::: ::	alignment_scores: Quality: 90.5 Ratio: 1.065 Percent Similarity: 43.59
126   IPheLeualaalaLeuPheProGlnPheIleMetProGlnGln 140	. BF
ProGInLeuMetGlnTyrIleValLeuGlyValThrThrIleVal 155	Align seg 1/1 to: BF52622 21 GlySerGlyAlaIleAsn 1  :::   ::     287 GGCAATGGAACTTCAAAT
540 ATAAGCTACTTCCTCATGGTCATCTTCATGAACTACAACGGTACCTCTG 589 163GlytytalaThrLeuGlytylalaThrLeu	35GlyTy   1     337 GGTGAGGCCTGTAGGCCA
	47 spargthrdlyaspserT    :::   ::   387 TGAGAAGTGGTTCACCA   64 PheSerArgSerVallie
177 GlyProLysGlnMetLysAlaLeuAsnLysIlePheGlySerLeu 191           ::: ::	428 GCAGATCTGTCCTCTTTC 76 pAlaGlyAlaAlaTyrLC 1 ::::::: 477 GAGGACCTCTGTTCATAI
entation_block:  ##E75220 774 bp mRNA EST 11-DEC-2000  ##60201237F1 NCT CRAP Brn64 Homo sapiens cDNA clone IMAGE:4214263	92 laAlaGlyAlaIleAspI ::: :::: 527 ACTGTAGAGGGATG
ACCESSION BF52620 VERSTON BF52620.1 GI:11613570 SOURCE human.	109 HisLeuPhedInArgAla ::::::    541TCCCAAGCI 121 nProLysSerlleValP
	582 CTCTCCGTGTGTCTGTGI 131LeuPhei 632 TGTGCAGGCTGTGTTTTC
Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: David N. Louis, M.D.	
CDNA Library Preparation: Lite Technologies, inc.  CDNA Library Arrayed by: The I.M.G.E. Consortium (LLNL)  DNA Sequencing by: Incyte Genomics, Inc.  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  http://inage.llnl.gov  Plate: LLAM9787 row: p column: 08	160 lMetileGlyTyralaT) 715
High quality sequence stop: 701. Location/Qualifiers	

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te_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
te_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
te_2: Sal1; Cloned this is a NCI_CGAP_Library."
lone c_231 g_196 t_1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheLeuAlaAla.....130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrLeuAlaGlnArgIleAlaLeuTrpIleLysG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JeulysserLeuAlaSerThrGlnSerArgArg 108
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SNTTGTTGTGTGTGTGAGGAGCACATCAGTG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGGGTGCCAG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrcysalaGlyTrpArgGlyValGlyThrLeu 63
                                                                                                                                                                                                                                                                                                                                                                                                                   eulleTrpLeuGly...IleGlnGlnTrpArgA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrProAlaGlyGlyValTyrCysTrpAlaSerA 47
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                                                                                                                                                                                                                                                                                                                                                                                                nThrMetThrThrSerLeuAsnHis..... 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eAlaPheGluValLeuLys.....Tr
                                                                                                                                                                                                                                                     Length: 195
Gaps: 8
Percent Identity: 25.128
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Uppublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF202399 438 bp mRNA EST 06-NOV-2000 WHE1768_B10_C202S Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE1768_B10_C20, mRNA sequence.
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Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
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378 IGTTGGGAGGGTATCCAGAAGAATTGTTGGAGGGTATCCAGAAGAATTG 329
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278 GTTCACCACATTTTCCTTTCTAAAATTTCTTGACCTGTCGTTAT
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                                                                                                                              ...TrpArgAlaAlaGlyAlaIleAspLeuLys.....SerLe
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328 TTGGGAGGTGGACCAGAATTCTGCACTGGAGGCCTACTCTGCATGTCTCT
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/Clone lib="GNN" out.2.
/Clone lib="GNN" out.2.
/Lissue_type="N2-fixing root nodules harvested one month post incoulation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR" it=1: ECORI; Site_2: /note="Vector: pBluescript SR*: Site_1: ECORI; Site_2: XhOI; cDNR was prepared from poly4+ enriched RNA from effective root nodules harvested one month post incoulation with Sinorhizobium meliloti. The cDNR was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Glappack III Gold packaging extracts. Plasmids containing cDNR inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR sequence name:MTCBW60TK
More information is available at. http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1..607
                                                                                                                                                                                                                       barrel medic.
Medicago truncatula
Medicago truncatula
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta: eudicotyledons; core eudicots; Rosidae; eurosids 1;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                      Peng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612-625-7219
                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 607)
Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Pe, H. Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
                                                                        AW980930 607 bp mRNA EST 07-SEP-2000 EST392083 GVN Medicago truncatula cDNA clone pGVN-60123, mRNA
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Gaps: 12
Percent Identity: 22.772
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/cultivar="genotype A17"
/db xref="taxon:3880"
/clone="pGVN-60123"
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Email: vance004@maroon.tc.umn.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Carroll P. Vance
                                                                                                                                                                            AW980930.1 GI:8172475
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0.918
48.020
seq_name: gb_est53:AW980930
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159 IleValMetIleGlyTyrAla 165
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/dultivar="Chinese Spring"
/dultivar="Chinese Spring"
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/dev_stage="Adult plant"
/lab_host="E. coll SOLR"
/dev_stage="Adult plant"
/lab_host="E. coll SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcorR; Site_2: Xhoi; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, and yellow anther were collected and total RNA, and polly(A) RNA were prepared, a CDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratgene SK primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 hrGlnSerArgArgHisLeuPheGlnArgAlaValPheValAsnLeuThr 120
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| 6 GACCGGGTACCGGATGCATAT...CAAGGGTGGCGGTCACGCTACTGCTC 52
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Percent Identity: 22.293
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                                                                      FEATURES
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) [pb] ARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampleillin resistance."
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Dunn,D., Adyadi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                         plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/\note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                             13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 E
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Gaps:
                                                                                                                                                       AZ601442 489 bp DNA
1M0419P08R Mouse 10kb plasmid UUGC1M
clone UUGC1M0419P08 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0419 row: P column: 08
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 489.
Location/Qualifiers
1. .489
                                                                                                                                                                                                                                                                           AZ601442.1 GI:11723632
372 GIGCIGGAGGICAAGIGGGCC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: plasmid ends
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                                                                     gb_gss24:AZ601442
                                                                                                                 seq_documentation_block:
LOCUS AFA1111
                                                                                                                                                                                                                                                                                                                                          house mouse.
Mus musculus
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HindIII"
121 c
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LOCUS BF043998
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Quality:
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                   165
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KEYWORDS
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                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ240216 511 bp DNA GSS 30-SEP-1998 CIT-HSP-2385F1.TF,1 CIT-HSP Homo sapiens genomic clone 2385F1, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 511)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a random human BAC End Sequence Database for Map Building
Unpublished (1998)
Other_GSSS: CIT-HSP-2385F1.TR.1
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                 295 GGGTCAATGCGAACACTCACTGGTCCCTACTCCACTGTCACCCAGGGG 246
                                                                                                                                                                                                                                                          245 AGCA......GCAGAGGAAGCGCCCAGGCCGCGGCGGCTGCAT 208
                                                                                                                                                                                                                                                                                                                                            207 ACTGGCCGGGGGTGGGCTCCTTGTCCTGAGCCCCTCAGGACCTACG 158
                                                                                                                                                                                                                                                                                                                                                                                 .....LeuPheSerArgSerValIleAlaPheGluVa 73
                                                                                                                                                                                                                   39 yGlyValTyrCysTrpAlaSerAspArgThrGlyAspSerTyrCysAlaG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 GlyalalleAsnThrMetThrThrSerLeuAsnHisGlyTyrProAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                          73 lLeuLysTrpAlaGlyAlaAlaTyrLeuIleTrpLeuGlyIleGlnGlnT
                                                                                                   to: 489
Percent Identity: 31.522
                                                                                                 Align seg 1/1 to reverse of: AZ601442 from: 1
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                   56 lyTrpArgGlyValGlyThr.....
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AQ240216
AQ240216.1 GI:3672414
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                                      alignment_block:
US-09-466-935-2 x AZ601442/rev
50.000
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LOCUS AQ240216
Percent Similarity:
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AUTHORS
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KEYWORDS
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Email: h-Lewinguiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Wonnack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 514)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA EST 10-OCT-2000 normalized bovine placenta Bos taurus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| :::||| 346 AGGATGAAGGAGTCCTTTGCGAGAGGCATGTTCTTGTGTGGGGTAGGTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 GCTCTGCACCAGGCATTTCTTCTTGTTTTCCTCTTCTCCTCTTCTGGGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 sGlyTyrProAlaGlyGlyValTyrCysTrpAlaSerAspArgThrGlyA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ThrLeuPheSerArgSerVallleAlaPheGluValLeuLys...TrpAl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 aGlyAlaAla.....TyrLeuIleTrpLeuGlyI 87
                                                                                                                                                                                                                                                                                                                                                                                                        18 LeuSerProGlySerGlyAlalleAsnThrMetThrThrSerLeuAsnHi 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 spSerTyrCysAlaGlyTrpArg......GlyValGly 61
                                                                                                                                                                                                                                                                                                                                                   to: 511
                                                                                                                                      Length: 88
Gaps: 6
Percent Identity: 30.682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone BP250014A20H3 5', mRNA sequence
BF043998
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      δ
114
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BP250014A20H3 SOares
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Unpublished (2000)
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Tel: 217 333 5998
Fax: 217 244 5617
                                                                                                                                                                           1.911
51.136
                                                                                                                                            86.00
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source
                                                AUTHORS
TITLE
JOURNAL
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                                   REFERENCE
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                                                                                               COMMENT
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Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                            seq_documentation_block:
LOCUS AL509238 623 bp mRNA EST 04-JAN-2001
DEFINITION AL509238 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare cDNA clone HY01C09u 3', mRNA sequence.
                                                                                                         1. :514
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/clone="BP250014A20H3"
/clone_llb="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 recedentecerracresaccresescentrecresecorganess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 TyrCysAlaGlyTrp...ArgGlyValGlyThrLeuPheSerArgSerVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 lileAlaPheGluValLeuLySTrpAlaGlyAlaAlaTyrLeuIleTrp.
                                                                                                                                                                                                                                                                                                                                                                                               Sercent Identity: 27.523
FORWARD: TAATACGACTAAAGG
BACKWARD: ATTAACCTCACTAAAG
INSERT LENGTH: 514 Std Error: 0.00
Plate: BP250014A20 row: H column: 3
Seq primer: AGCGGATAACAATTCACACAGGA
High quality sequence stop: 514.
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to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 ......GGAAGGAGCAT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
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AL509238.1 GI:12035741
                                                                                                                                                                                         /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                               1.755
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                                                                                                                                                                                                                                                                                                                                                                                86.00
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US-09-466-935-2 x BF043998
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                                                                                                                                                                                                                                                                                                                                                                             Quality:
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Percent Similarity:
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KEYWORDS
SOURCE
                                                                                             FEATURES
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/tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="%AtOLR"
/lab_host="VetOr: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
/note="VetOr: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
Xhoī; mRNA was made from developing caryopsis (3.-15.DAP)
of spring barley variety 'Barke', a high quality malting
variety. Cloning sites: EcoRI (5'-end of CDNA), and Xhoī
(3'-end of CDNA). NOTE: Due to a cloning artefact caused
by the kit, in most cases the EcoRI site is NOT present,
as well as the EcoRI adapter. Average insert size is 1 kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp"
26 a 150 c 166 g 179 t 2 others
                                        Hordeum.

I (bases 1 to 623)

Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.

EST sequencing and analysis in barley
Unpublished (2000)

Contact: Michalek W

Institute for plant Genetics and Crop Plant Research

Corrensstr.3, D-06466 Gatersleben, Germany

Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de

Seq primer: Misun primer for 3'end.
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_llb="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::|||::: ||||
160 ACAGCACAGCGACCATATATAGGGCTAGCAGCTGTTCTTTTAGGGACGG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....TACTGCTCG 232
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30002300.00+00 to 10002	45 aSer
seq_uame: yo_estyo:setoryous	 424 CTCGGCCTTGTC
DEFINITION 60215419F1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4295405 5',	47As
ACCESSION BF679835 VERSION BF679835.1 GI:11953644 KEYWORDS EST.	60 ValGlyThrLeuk
×	524
	76 palaglyalaala  :::         535 gagagagagana
	92 aAla
JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Tel: (301) 466-1550	   579 GGCGAAGCTCAA
Email: Robert Strausberg@nih.gov Tissue Procurement: CLONETECH Laboratories, Inc. CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be	98 eulysserleuh. 
	131 uPheProGlnPh               ::   699 GTTCCTGGGTG
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full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."  BASE COUNT 159 a 289 c 311 g 218 t  ORIGIN	
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Align seg 1/1 to: BF679835 from: 1 to: 977	
<pre>3 LeuGlurrpTrpPheAlaTyrLeuLeuThrSerIleIleLeuThrLeuSe 19 ::::::        :::::    ::::   ::::   ::::    274 ArgrCrrGGGCTrTCrCCrGArGACCGAGGACTACTGGTGTTTTC 323</pre>	
19 rProGlySerGlyAlalleAsnThrWetThrrhrSerL 32              :::::::::::::::::::::::::	
32 euAsnHisGlyTyrProAlaGlyGlyValTyr.CysTrpAl 45	

45	aSer	46
424	CICGGCCTTGTCATCCTCCACAAAGAGCAGCTTGGCAAAGCCCACCTGGT	473
47		59
474	TACGCGGCATGGGCAGGCTGCTGGCTGTTGCTGGGCAGGCTGCA	523
9	ValGlyThrLeuPheSerArgSerValIleAlaPheGluValLeuLySTr	97
524		534
16		92
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92	aAlaGlyAlaileAsp	86
579	GGCGAAGCTCAAGCTATACCATGCTACTT	628
86	euLysSerLeuAlaSerThrGlnSerArgArgHisLeuPheGlnArgAla	114
629		663
115	ValPheValAsnLeu	131
664		869
131		
669	GITCCCTGGGTGGTTTATGCCCTGGTCTCACCAGGTTGGTCATTAT 744	

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AX030177 Sequence
AE000458 Escherich
AE005613 Escherich
AC073768 Mus muscu
AC020970 Mus muscu
AC020916 Mus muscu
AC079167 Mus muscu
AC079167 Mus muscu
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AC087563 Homo sapi AC022157 Homo sapi AC022157 Homo sapi AC028784 Muss muscu AE006110 Pasteurel AE004719 Pseudomon AE004109 Vibrio ch AF235020 Brucella U32810 Hacemophilus AX030079 Sequence AC000140 Escherich Z47200 Yersinia en U7387 Escherichia AE004589 Pseudomon ME004889 Pseudomon U04992 Pseudomonas AF087482 Pseudomonas AF087482 Pseudomonas AF087482 Pseudomonas AF08759 Pseudomonas AF0876121 Bacillus AE005212 Escherich	AE004864 Pseudomon AX063725 Sequence AC052017 Homo sapi Continuation (21 o AC073621 Homo sapi AC004928 Homo sapi AC064928 Homo sapi AC06540 Ectshmani L27597 Human CD79b AE006140 Escherich AC071237 Glardia i AC071237 Glardia i AC071237 Gsequence AE000274 Escherich D90824 E.coli geno	16-SEP-2000 : Enterobacteriaceae;	Tokhmakova, I.L. and	PDPFFVSQTAVSRSRKEAMMGVLG GLYLCWMCYQMLRGALKREAVSAP SLEVGDNVGTTARWGIFALIIVET FAGFGIHLIISR"
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; I (bases I to 11509)

I (bases I to 11509)

Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Qravfvultupksivflaalfpqfimpqqpqimqyiviggvitivudiivmigyatlaq
Rialwikgpkomkalnkifgslfmlvgallasarha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="f138; 100 pct identical to YIGK_ECOLI SW: P27847" /codon_start=1
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/note="RRP (repetitive extragenic palindromic) element;
contains I RRP sequence"
complement(3654. 4070)
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3244. 3592. 35947.
/gene="yigJ"
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             1019. 1047
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1077. 2909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="o610; 99 pct identical to 607 amino acids ofRECQ_ECOLI SW: P15043 but has 3 additional N-ter
                                                                                                                                                                                                                                                                                                                                   /EC_number="3.6.1.-"
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restriction/modification"
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3224. 3592
/gene="YigJ"
/function="orf; Unknown"
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                                                                                                                                                                                                         /note="b3822"
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Plunkett,G. III.

Bliect Submission

Submitted (13-077-1998) Laboratory of Genetics, University of Submitted (13-077-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

This sequence was determined by the E. Coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants H60301 and H601428 (from the Human Genome Project and NCHGR). The entire sequence was independently Getermined from E. Coli K12 strain MG1655. Predicted open reading frames were determined using Genemark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with Genet correlated with Genes in the E. Coli Genetic Site Nos., unique ID nos. for the genes in the E. Coli Genetic Site Nos., unique ID nos. for the genes in the E. Coli Genetic Site Nos., unique ID nos. for the genes in the E. Coli Genetic Site Nos., unique ID nos. for the genes in the E. Coli Genetic Site Nos., unique ID nos. for the genes in the E. Coli Genetic Organic Arguments of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. Coli (http://www.genetics.wisc.edu). Annotation of the genome is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Requence described in reference I. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of or angene agene agene or and labels. This should allow them to be searched for in Bntrez as gene
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EHDNPFT1YPYDTWTLIYTGTSDLMKEAIASYDWABNARNBEVKFGDISLAFPLWRGIL
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IGYHLGDAVLSAKGQYNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFNQ
                              Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
                                                                                                                                                                                                                                                                                                                           Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorus compounds" /note="0289; 99 pct identical to PAl_ECOLI SW: P00631; CGSCNO. 384"
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/product="outer membrane phospholipase A"
/protein_id="AAC76824.1"
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/sub_strain="MG1655"
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                                                                                                                                                                                                     3 (bases 1 to 11509)
Blattner, F.R.
                                                                                                                                                                                                                                                                                                Direct Submission
        Submission
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FVRFRAQHHDRVVVICPGRIESYVKYAELAYDLFHLGFDVLIIDHRGGGRSGRLLADP
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MHDRFCELRTAAGHPVEGGRPLVIKGAYHEILFEKDAMASVALHAIVDFFNRHNSPSG
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5426. .545
/note="factor Sigma70; predicted +1 start at 4007854"
5438. .546
/note="factor Sigma70; predicted +1 start at 4007865"
5494. .5523
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                                                                                                                                                                                                                                                                                                                                              /note="0340; 99 pct identical amino acid sequence and equal length to PLDB_ECOLI SW: P07000"
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start at 4006612'
                                                                                   Central intermediary metabolism:
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Pred. No. 3.9e-167;
0; Mismatches 0; Indels 1
 <del>+</del>
                                                                                                                                                          /product="lysophospholipase L(2)"
/protein_id="AAC76828.1"
predicted
 Sigma70;
                                                                                                 Phosphorus compounds"
                                                                                                                                                                                     /db_xref="GI:2367303"
                                                                       /EC_number="3.1.1.5"
                                                                                    function="enzyme;
                                                                                                                                               /transl_table=11
                                                                                                                                     /codon_start=1
/note="factor
1384, .5406
                                    /note="b3825"
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99.8%;
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/gene="yigL"
                                                 1384. .5406
/gene="pldB
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On May 29, 1995 this sequence version replaced gi:148169.
This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Misconsin-Madison. The entire sequence was independently determined from E. coli MG1665. Overlaps and conflicts with other sequence determinations are annotated. Reference [1] describes the original sequence determination of a 91408 bp sequence. References [2], [3], and [4] describe subsequent corrections and/or updates to that
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/map="bp l at 3974 kb; 84.7 minutes"
/note="filths sequence comprises the following lambda clones: DD650(ECL15-116), DD651(ECL3RM4), DD854(ECL5-177), DD856(ECL9RM8.1), DD858(ECL7RM9),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (bases 1 to 91414)
Rudd,K.E., Sofia,H.J., Koonin,E.V., Plunkett,G. 3rd, Lazar,S. and
Rouviere,P.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Daniels,D.L.
Direct Submission
Direct Submission
Submitted (12-FEB-1992) Donna L. Daniels, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu; Phone: 608-262-2534; Fax:
                                                                                                                                                                                                                           E. coli genomic sequence of the region from 84.5 to 86.5 minutes. W87049.1 GI:836656
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Chases 1 to 91414)
Plunkett, G. III., Burland, V., Daniels, D.L. and Blattner, F.R. Analysis of the Escherichia coli genome. III. DNA sequence of region from 87.2 to 89.2 minutes
Nucleic Acids Res. 21 (15), 3391-3398 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daniels,D.L. Plunkett,G. III., Burland,V. and Blattner,F.R. Daniels,D.L., Plunkett,G. III., Burland,V. and Blattner,F.R. Analysis of the Escherichia coli genome: DNA sequence of the from 84.5 to 86.5 minutes Science 257 (5071), 771-778 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence of
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Blattner, F.R., Burland, V., Plunkett, G. III., Sofia, H.J. and
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Analyzis of the Escherichia coll genome. IV.
Analyzis of the Booterichia coll genome. IV.
Proglon from 89.2 to 92.8 minutes
Nucleic Acids Res. 21 (23), 5408-5417 (1993)
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/organism="Escherichia coli"
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/LTAISLALION-"MHINVTQGGLMSLSIVHTRAALGVNAPPITVEVHISKGLPGLTM
VGLPETTVKEARDRYBRAIINSGYEYPAKKITINLAPADLPKEGGRYDLPIAIALLAA
SEQLTANKLDEYELVGELATGALERGYPGASISSATBAKSGRRIIVAKNDEBEYGLIN
GEGCLTADHLQAVCAFLGSKRALEXRYFTDAVSRALQHDLSDVIGGDGGKRGLEITAA
GGHNLLLIGPPGTGKTMLASRINGLLPDLSNEBALESAAILSLVNABSVQKORRORP
ESPHSAKALTANYGGAAIPGPCBISIAHNGVLELDELPEFERRILDALREPTESGOIH
ILSTRAKITYPARFGLVAAMNPSTGHYQGHNRCTPEQTLRYINLSGPFLDRFDLS
LEIPLPPPGILSKTVVPGESSATVKQRYMAARRRQFKRYGNKLNAWLDSPEIROFCKLE
SEDAMULEGTLIHLGLSIRAWGRLLKVARTIADIDGSDIITRQHLQBAVSYRAIDRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mnGaQwvVHaLRAQGVNTVFGYPGGAIMPVYDALYDGGVEHLLC
RHEQGAAMAAGYARATGKTGVCIATSGPGATNLITGLADALLDSIPVVAITGQVSAP
FIGTDAPGPVDVLGLSLACTKHSFLVQOSLEELENARARPVACSGREGPVLVDIPKD
IQLASGDLEPRFTTYENEVYRPHAEVEQARQMLAKQKPMLYVGGGVGMAQAVPALRE
FLAATKMPATCTLKGLGAVEADYPYYLGMLGMHGTKANFAVOECDLLIAVGARFDDR
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/protein_id="AAA67571.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603; inactive in wild-type E. coli K12"
                                                      /note="similar to Mg chelatase subunit of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="the mutation ilv02096 joins this ORF to ilvg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MTALLRVISLVVISVVVIIIPPCGAALGRGKA" 3696. 4679
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/protein_id="AaA67570.1"
/db_xref="G1:148174"
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/note="predicted bend of 79 degrees"
3297...3326
/note="promoter matrix score of 74"
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/note="corresponds to V00289 (1.
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/note="corresponds to M11651 (1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3379. .5721
/note="700290; ECILVX(1. .2343)"
3458. .3556
/gene="11vL"
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                                                                                                                                      /function="unknown"
/protein_id="AAA67569.1"
                                                                                                                                                                              /db_xref="GI:148173
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/transl_table=11
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/codon_start=1
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/qene="ilvL"
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/gene="o221"
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/gene="o221"
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RAGNGSLWYKQLHERQLDLITTERARKMDEFSSQLLGYFTLALYTSAPSKLKGDLNYL
RLEWGPDFQQHEAGLIGADBYPILTTSSAELAQOQIAMLNGCTWLPVSWARKKGGLHT
VVDSTTLSRPLYAIWLQNSDKNALIRDLLKINYLDEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAA67567.1"
/db_xref="G01:148171"
/translation="MDTELLTFLEVSRTRHFGRAAESLYLTOSAVSFRIRQLENQLG
VNLFTRHRNNTRLTAGEKLLLPYAETLMSTWQAARKRWRIPHDITSFLSVPAPRCGNV
CLISGWDACIKIRMPIQAYSSKRELPNGSLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAESFTTTNRYFDNKHYPRGFSRHGDFTIKEAQLLERHGYAFNE
LDLGKREPVTEEEKLFVAVCRGEREPVTEAERVWSKYMTRIKRPKRFHTLSAVNRRLK
VLKTTPILTINKKGEMPFFYVSSFCRWMSKRSIAR"
DD861(EC17-221),DD864(EC27-149), DD865(EC21-76),
DD867(EC27-860). M13mpl9 or Janus vectors were used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    possible pssR gene"
                                                                                                                                                                                                         'note="corresponds to V00349 (164. .500)"
                                                                                                                                                               note="corresponds to M37337 (1. .4900)"
                                                                                     .200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253. .396
/note="predicted bend of 81 degrees"
complement(266. .862)
/gene="f198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted bend of 77 degrees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151. 1179
/note="promoter matrix score of 57"
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                                                                                 note="corresponds to K02846 (1.
                                                                                                                                                                                                                                                                                                                                                                                                                          177. .205
/note="terminator-like sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="0137"
/hote="terminator-like sequence"
complement(1585. .3135)
/gene="f516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA67566.1"
/db_xref="GI:148170"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="CGSC No. 18010;
                                                                                                                         /note="clone EC15-116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(703. .1104)
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/gene="f133"
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/gene="f198"
                                                                                                                                                                                                                                                                   1686
                                                                                                                                          .4899)
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/function="unknown"
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                                                                                                                                                                                                                                                                                                                        95. .170
/gene="trpT"
/note="CGSC No. (
                                                                                                                                                                                                                                               /gene="aspT"
/note="CGSC No.
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888"
2881 ILCLFLLCCIYNLWTLRPVQILYTYSDAGNSVFLVV
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AVINEYPYRNTHIGINDFTEYQLTQENKIEQVFNPHNFKK
                                                                                                                                                                                                                                        nown function"
o 131 of 254 are 95.41 pct identical to
f 161 from Escherichia coli K-12 Strain
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RANGEAWGTLHALLADMNSQGQVQMAMNGGIYDESYAPLG
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PWQRYPFVTMISVERKG"
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11 K-12 MG1655"
1689)
                                                                                                                    5; Region of the EDL933 chromosome not li K-12 MG1655"
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(6 of 316 from Escherichia coli K-12
.6"
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nia coli 0157:H7"
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int matches"
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Pred. No. 3.9e-163;
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ilarity 97.4%;
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AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

ACCESSION VERSION KEYWORDS

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Direct Submission
Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Estimated insert size: 212936; sum-of-contigs estimation Estimated insert size: 157000; pulse field gel estimation Quality coverage: 4.20x in Q20 bases; pulse field gel estimation Quality coverage: 3.10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 10
                                                                                                                                                                                                                           ACU20970 212936 bp DNA HTG 10-FEB-2000
Mus musculus clone RP23-252M21, WORKING DRAFT SEQUENCE, 144
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 144 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
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-----Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
I (bases 1 to 212936)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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JOURNAL
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SOURCE
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/db_xref="taxon:10090"
/db_xref="Rexon:10090"
/clone="RP23-359N18"
/clone="RPC3 Rouse BAC library 23"
68608_1b="RPC1 mouse BAC library 23"
                                                                                                                                                                                                              unknown length of 12045 bp in '
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contig of 29530 bp in length.
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Pred. No. 1.1e-152;
0; Mismatches 3;
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of 26817 bp in
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comptement(1506. .2334)

fgene="STMD1.99"

//mote="STMD1.99"

//rne="STMD1.99"

//rrPa) (SP:P22788) and 95% identity with amino acids 1-80

of E. coli possible regulatory protein (PSSR) (SP:P27826)"
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similarity to Pfam family
subunit ChlI), score=351.8,
                                                                                                       Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs GLIMMER (Salzberg, S., Delcher, A., Kasif, A. and White, O. (1998 NAR 26,544-548), and GeneMark (Lukashim, A.V. and Borodovsky, M. (1998), NAR 26,1107-1115.
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such as compressions and repeats; all regions were covered sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                  /organism="Salmonella typhimurium LT2"
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Submitted (09-FEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
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                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctggcgtggtttaccgtcgttgccagcctgtttgccctgccgcaaatgcgccgtggttat 540
  cccgatttcttttttgtctctcagaccgctgtcagtcgttcccgtaaagaagcgatgatg 120
                                                                               ggcgtgctggggcattacctgcggcgtaatggtttgggctgggattgcgctgcttggcctg
                                                                                                                                                                                                                                              tatctctgctggatgggttaccagatgctacgtggtgcactgaaaaaaagaggggtttct
                                                                                                                                                                                                                                                                                                                              gcacctgcgccacaggtcgagctggcgaaaagtgggcgcagtttcctgaaaggtttactg
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St. Louis, MO 63110, USA
e-mail: sclifton@watson.wustl.edu or
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Washington University Genome Sequencing Center.
The Salmonella typhimurium Genome Sequencing Project
Unpublished
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Salmonella typhimurium fragment STMD1.
AF233324
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4934. .6580

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II (ILVG) (SF: P00892) ; contains similarity to Pfam

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score=922. & E=1.8e-295, N=1"

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6858. .7787
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ARDRVRSAI INSGYEFPAKKITINLAPADLPKEGGRYDLPIAVALLAASEQLTASNLE
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SHKGPVVFRHREHMQRLRDSAKIYRFPVSQSIDELMEACRDVIRKNNLTSAYIRPLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="100% identity to E. coli ilvGMEDA operon leader peptide (ILVL) (SP:03060)"
/protein_id="AAR33486.1"
/db_xref="GI:6960296"
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fyrotein id="AAR33481.1"

/db_xref="G1:6960291"
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ALITDGRESGGTSGLSIGHVSPEAASGGTIALIEDGDTIAIDIPNRSIQLGSBAEIA
ARREAGERAGDKAWTPKNRQRQVSFALRAYASLATSADKGAVRDKSKLIGG"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 266294)
DOE Joint Genome Institute.
                                                        ACO20885 268294 bp DNA HTG 16-FEB-2000 Mus musculus clone RP23-46411, LOW-PASS SEQUENCE SAMPLING.
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gap of unknown length
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Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R., Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R., Ishikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J. S. and Kucherlapati, R., Direct Submission, J. S. and Kucherlapati, R., Direct Submission G.J. S. and Kucherlapati, R., Bristein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
On Aug 30, 2000 this sequence version replaced gi:9885883.
Albert Einstein College of Medicine Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 290452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome 6 clone RP23-226D23 strain C57BL6/J, *** SEQUENCING IN PROGRESS ***, 196 unordered pieces.
* NOTE: This is a 'working draft' sequence. It currently consists of 196 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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High Throughput Mouse Sequencing
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**Estimated insert size: 286552 - sum-of-contigs
Quality coverage: agarose-FP - N/A
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bin/ws.exe/mouseDB/mouseSEQ/mouseseqtable.hts
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Chemistry: Dye-terminator Big Dye; 1008
Cconsensus quality: 196511 at least 020
*Consensus quality: 173308 at least 030
*Consensus quality: 138790 at least 030
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house mouse.
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852: contig of 852 bp in length

33181 34033: contig of 853 bp in length 34034 34053: gap of unknown length 34972: contig of 919 bp in length 34973: 38975: contig of 883 bp in length 358976: 358975: contig of 883 bp in length 358976: 35971: contig of 883 bp in length 358976: 35712: contig of 888 bp in length 36752: 37639: contig of 888 bp in length 36752: 37639: contig of 880 bp in length 37640: 37639: gap of unknown length 38519: gap of unknown length 38520: 3348: contig of 829 bp in length 38520: 3348: contig of 829 bp in length 40378: contig of 829 bp in length 40378: contig of 882 bp in length 41470: 41469: contig of 1072 bp in length 41470: 41469: contig of 1072 bp in length 41470: 41469: contig of 1072 bp in length 41470: 41469: contig of 1072 bp in length 41470: 41469: contig of 885 bp in length 41877: contig of 884 bp in length 42795: contig of 884 bp in length 42795: contig of 884 bp in length 42877: contig of 884 bp in length 42877: contig of 884 bp in length 42877: contig of 884 bp in length 42877: contig of 884 bp in length 4298: gap of unknown length 42998: contig of 884 bp in length 42918: gap of unknown length 42918: gap of unknown length 42919: contig of 885 bp in length 42918: gap of unknown length 43917: gap of unknown length 43918: 51054: contig of 885 bp in length 43918: 51054: contig of 885 bp in length 51075: 51074: gap of unknown length 51075: 51074: gap of unknown length 5208: 51074: gap of unknown length 5208: 51074: gap of unknown length 5208: 51074: gap of unknown length 5208: 51074: gap of unknown length 5208: 51074: gap of unknown length 5208: 51074: gap of unknown length 5208: 51074: gap of unknown length 5208: contig of 575 bp in length 5208: contig of 675 bp in length 5208: gap of unknown length 5208: gap of unknown length 5208: gap of unknown length 5208: gap of unknown length 5208: gap of unknown length 5208: gap of unknown length 5208: gap of unkn	55273: gap of 55273: gap of 55527: cont.ig 56547: gap of 57376: cont.ig 57376: cont.ig 57376: cont.ig 57473: cont.ig 58377: cont.ig 58377: gap of 58377: gap of 59288: cont.ig 59288: cont.ig 59289: cont.ig 60519: gap of 60519: gap of 62752: cont.ig 62752: cont.ig 63643: gap of 63643: cont.ig 63643: gap of 64694: cont.ig 63643: gap of 64694: cont.ig
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KIGYHLGDAVLSAKGQYNWNTGYGGAELGLSYPITKHYRLYTQVYSGYGESLIDYNFN
                                                                                              Db 104019 GTAAAGATTNNNNNNNNNNNNNNNNNNNNNNNNTACGTGGTGCACTGAAAAAGA-GCGGTTTC 104077
                                                                                                                      Db 104318 TCAACGTCTGGCGAAGTGGATTGATGGTGTTTGCCGGGGCGTTATTTGCCGGATTTGCCAT 104377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                       240 gtatctctgctggatgggttaccagatgctacgtggtgcactgaaaaaagaggcggtttc 299
                                                  Gaps
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E.coli recQ gene complete cds, and pldA gene, 3' end.
M30198
M30198.1 GI:147557
                                                                                                                                                                                                                                                                                                                        tcaacgtctggcgaagtggattgatggttttgccggggcgttatttgccggatttggcat
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Irino, N., Nakayama, K. and Nakayama, H.
The recQ gene of Escherichia coli K12: Primary structure evidence for SOS regulation
MO1. Gen. Genet. 205, 298-304 (1986)
87115164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detergent-resistant phospholipase A; phospholipase; pldA
                                                1;
                       Length 290452;
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Pred. No. 1.4e-88;

    2695
/organism="Escherichia coli"
/strain="K-12"

                                              0; Mismatches
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Escherichia coli
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479. .2311
                                   al Similarity 93.1
353; Conservative
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PABAMLFYDPADAMAURRCLEEKPQGLQDIERHKLNAMGAFAEAQTCRRLVLLNYFG
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LQLAPPRIYALLKRAMQKSFGGNYDRKLFAKLRKRSIADESNVPPYVVFNDATLIE
MAEQMFITASEMLSYNGVGRKELEREGKPFMALIPAHVDGDDEE"

MAEQMFITASEMLSYNGVGRKELEREGKPFMALIPAHVDGDDEE"
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DOE Joint Genome Institute.
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Mus musculus clone RG-MBAC_40H2, LOW-PASS SEQUENCE SAMPLING.
ACO20833
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Louis denome Institute.

Direct Submission
Louis denome Institute.

Louis treet Submission
Louis denome Institute, 2800 Mitchell Drive, Walnut Creek, CA 945;

* NOTE: This record contains 69 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tatctctgctggatgggttaccagatgctacgtggtgcactgaaaaaagaggcggtttct
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Pred. No. 5.1e-76;
0; Mismatches 2;
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/codon_start=1
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HTG; HTGS_PHASE0.
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Best Local Similarity 98.8%;
Matches 319; Conservative
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DOE Joint Genome Institute.
Direct Submission
Submitted (10-JAN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
------Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 298166)
Dobb Joint Genome Institute.
Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 189570 bases at least Q40
Consensus quality: 207567 bases at least Q30
Consensus quality: 277222 bases at least Q30
Consensus quality: 277222 bases at least Q30
Estimated insert size: 231000; agarose-fp estimation
Estimated insert size: 230766; sum-of-contigs estimation
Quality coverage: 8.11 in Q20 bases; agarose-fp estimation
quality coverage: 6.44 in Q20 bases; aum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                            10815 TGTCGGTGATAACGTTGGCACTACCGCGCGCGCATTTTTGCGCTGATCATTGTCA 10756
                                                                                                                                                                                                                    357 actgaccaatctcgctaatccgaaagcgattatctactttggctcggtgttctcattgtt 416
                                                                                                                                                                                                                                                                                                 417 tgtcggtgataacgttggcactaccgcgcgctggggcatttttgcgctgatcattgtcga 476
                                                                                                                                                                             0; Gaps
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                                                                                                                                         Length 62274;
                                                            341 others
                                                                                                                                     Ouery Match 39.3%; Score 242.8; DB 66; Length Best Local Similarity 95.4%; Pred. No. 2.4e-60; Matches 250; Conservative 0; Mismatches 12; Indels
/organism="Mus musculus"
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/clone="RG-MBAC_40H2"
| 13547 c 13251 g 18170 t
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Center Project Name: 0
Center clone name: RPCI-11_358F6
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AC087563.1 GI:12061429
HTG; HTGS_PHASE1; HTGS_DRAFT.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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DOE Joint Genome Institute.
Direct Submission
Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4950 165049: contig of 19201 bp in length
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8404 198503: gap of unknown length
8704 243778: contig of 44875 bp in length
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1379 298166: contig of 54688 bp in length
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/clone="Ib="RPCI human BAC library 11"
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DOE Joint Genome Institute.
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Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 265383)
DOE Joint Genome Institute.
Sequencing of Mouse
 Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mus musculus clone RP23-333M14, LOW-PASS SEQUENCE SAMPLING.
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                                                                                 * NOTE: This record contains 8 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Pred. No. 2.4e-24;
0; Mismatches 10; Indels 3
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2829: contig of 108 bp in length
gap of unknown length
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gap of unknown length
1566: contig of 730 bp in length
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                                                            Web site: http://www.jgi.doe.gov
                 Center: Joint Genome Institute
Center Code: JGI
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HTG; HTGS_PHASE0.
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Direct Submission
Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
On Feb 16, 2000 this sequence version replaced gi:6686434.
* NOTE: This record contains 244 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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DOE Joint Genome Institute.
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Pasteurella multocida
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
1 (bases 1 to 10184)
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Pasteurella multocida PM70 section 77 of 204 of the complete
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contig of 771 bp in length gap of unknown length contig of 641 bp in length gap of unknown length contig of 826 bp in length gap of unknown length gap of unknown length contig of 298 bp in length gap of unknown length contig of 624 bp in length gap of unknown length gap of unknown length contig of 998 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 1329 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 834 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 834 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 229 bp in length gap of unknown length gap of unknown length contig of 135 bp in length gap of unknown length gap of unknown length contig of 135 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length
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                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. (2001) In press
2 (bases 1 to 10184)
Zhang.O. and Kapur.V.
Direct Submission
Submitted (24-OCT-2000) Department of Veterinary Pathobiology,
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
                  Zhang,Q., Li,L., Paustian,M.L., Whittam,T.S. and
                                                                                                                                                                                                                                                                                                                                                /organism="Pasteurella multocida"
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Kapur, V.S.
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                               AUTHORS
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Pred. No. 6.5e-15;
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	Description	E. coli L-threonin	Escherichia coli y	Stealth virus nucl	Escherichia coli y	Gene encoding a su	A. vitis hypersens	A. vitis hypersens	Human ORFX ORF1040	Photorhabdus lumin	Neisseria gonorrhe	Stealth virus nucl
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            Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced Rhtc protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
                                                                                   The present sequence is the L-threonine resistance gene, rhtC, from Escherichia coli. This sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-homoserine, L-valine and L-leucine at increased levels.
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Pred. No. 4.1e-193;
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The present sequence is the yahN gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                         production of L-amino acids by an Escherichia bacterium increasing the expression amount of an L-amino acid excretion
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Pred. No. 4.5e-08;
0; Mismatches 307;
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                                 gtgggcgcagtttcctgaaaggtttactgaccaatctcgctaatccgaaagcgattatct
                                                          371 ggtatgtcttttttcgccgcggattaattaccgatctctctaacccgcaaaccgttttat
                                                                                                        431 tttttatcagtattttctcagtaacattaaatgccgaaacaccaacatgggcacgtttaa
                                                                                                                                 gcatttttgcgctgatcattgtcgaaacgctggcgtggtttaccgtcgttgccagcctgt
                                                                                                                                                                                ttgccctgccgcaaatgcgccgtggttatcaacgtctggcgaagtggattgatgtttg
                                                                                  actttggctcggtgttctcattgtttgtcggtgataacgttggcactaccgcgcgctggg
                                                                                                                                                        tggcctgggggggattgtgctcgcatcaattatctggcgagtttttcttagtcaggcgt
                                                                                                                                                                                                                                                                                                                                                                                                             Stealth virus; detection; diagnosis; infection; ss
                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO: 22.
                                                                                                                                                                                                                              572 ccggggcgttatttgccggatttggcattcatttgatt 609
                                                                                                                                                                                                                                              Location/Qualifiers
8118
                                                                                                                                                                                                                                                                                                                                                                                       Stealth virus nucleic acid clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US27744.
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                                                                                                                                                                                                                                                                                                                X84330 standard; DNA; 8387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MART/) MARTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    Stealth virus
                                                                                                                                                                                                                                                                                                                                                              08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                       X84330;
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X84330/
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This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 corn more contiguous nucleotides identical to sequence previously identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA which a molecular probe that method is used to detect stealth virus in a biological product, food or in the environment. The method is also used to evaluate agents for their cinhibitory or stimulatory effects on stealth virus replication and to cherential capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNAYTKNDWNANDTYCTYTATHIDKIKYNTVGHNNNNCDMKNYSABWRNTDWGAATTCGT 8107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8346 SNKHTSYAAMVKGCWNATKYNRYTKKSANKGHNATKYNRYTKKSANKGHHYWVTASTRYA 8287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8286 NAYNKMDHGVINTIHVGVNTHCHAAGVVHGGDHHYWASYGKNAYIKNDWTKYNNAYIKND 8227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acgiggigacacigaaaaaaaaagagggitticigcaccigcgccacaggicgaggiggaa 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctactttggctcggtgttctcattgtttgtcggtgataacgttggcactaccgcgcgctg 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 ggtttggggctgggattgcgctgcttggcctgcatttgattatcgaaaaaatggcctggct 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli; yeas gene; amino acid production; excretion protein gene; amino acid excretion protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     geatacgetgattatggtgggeggtggectgtatetetgetggatgggttaceagatget
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8387;
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8387 BP; 1807 A; 2320 C; 2218 G; 1844 T; 198 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 36.2; DB 20; 23.5%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.2;
87; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gggcatttttgcgctgatcattgtcga 476
                                                      Claim 19; Page 61-64; 95pp; English.
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                 Novel strains of stealth virus
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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ID A5
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(MIZU/) MIZUNO K.
(OJIP ) OJI PAPER CO.
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                                                                              P-PSDB; Y85179
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                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the yeaS gene (an excretion protein gene) of Scherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alamine, valine, histidine, isolaucine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 cgagctggcgaaaagtgggcgcagtttcctgaaaggtttactgaccaatctcgctaatcc 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 gaaagccattttgttctatgtgtcgtttttcgtacagtttatcgatgttaatgccccaca 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.6%; Score 34.8; DB 21; Length 639; 50.6%; Pred. No. 0.16; ive 0; Mismatches 82; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellulose production; increase yield; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           taccgcgcgctggggcatttttgcgctgatcattgtcgaaacgctg 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 tacgggaatttcattcttattctggcggcgacgctggaactggtg 489
                                                                                                                                                                                               Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 639 BP; 142 A; 128 C; 161 G; 208 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene encoding a subunit of cellulose synthase.
                                                                                                                                                                                               Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 19-20; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                              99EP-0125263
                                                                                                             98RU-0124016.
                                                                                                                                                                                               Zakataeva NP,
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A10594 standard; DNA; 10732
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nes 84; Conservative
                                                                                                                                                             (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                              WPI; 2000-414802/36.
P-PSDB; B01787.
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                                                                                                                                                                                            Livshits VA,
Tokhmakova IL;
            EP1016710-A2
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                                                                           17-DEC-1999;
                                                                                                                             09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1998;
                                                                                                             30-DEC-1998;
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                                            05-JUL-2000
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Matches
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A10594/
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This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits of cellulose synthetic equipment, that can be used to increase the amount of cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9728 AYDACYDAYDANCYSSDSTYTBYCSRRCCCYYDAYSCSRYDARCYDACYSYSNSTCYDAT 9669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene encoding a cellulose synthetic equipment – for the improvement the amount of cellulose synthesised in a plant body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 gettatgageeceggteecgatttettttttgteteteagaeegetgteagtegtteecg 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 taaagaagcgatgatgggcgtgctgggcattacctgcgggcgtaatggtttgggctgggat 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 tgcgctgcttggcctgcatttgattatcgaaaaatggcctggctgcatacgctgattat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypersensitive response elicitor protein; HR, disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9608 TBYSSRSRGYSYCSRSRCYSCYTDSDSTCYSTTYSTTYAYSCTTSRGYSYD 9556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 ggtgggcggtggcctgtatctctgctggatgggttaccagatgctacgtggtg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
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P-PSDB; B11630, B11631, B11632, B11633, B11634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.6%; Score 34.8; DB Best Local Similarity 15.9%; Pred. No. 0.65; Matches 37; Conservative 101; Mismatches
                                                                                                                                         Claim 2; Page 14-21; 32pp; Japanese
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A61501/C
ID A61501 standard; DNA; 1668 BP
XX
AC A61501;
XX
DT 23-OCT-2000 (first entry)
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(CORR ) CORNELL RES FOUND INC

99WO-US26079. 98US-0107387.

05-NOV-1999; 06-NOV-1998;

18-MAY-2000

Herlache TC, Zhang

Burr TJ,

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Agrobacterium vitis Pypersensitivity response (HR) elicitor proteins advances elections that is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis in walling-off and killing of the pathogen. On grape plants, the A. vitis of plant cells and induction of pathogen resistence. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to proteins, in non-infectious form, are used to treat plants or their seeds to proteins, in non-infectious form, as those caused by fund, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to cold, and to improve nutritional value, e.g., altered oll content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and the proteins of previously untreatable diseases; provide systemic treatment; and the proteins of previously untreatable diseases; provide systemic treatment;
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                       New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production
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                                                                                                                                                                          Sequences A61501-A61524 represent nucleotide sequences encoding
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Pred. No. 0.75;
0; Mismatches 116;
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                                                                                                                          Claim 7; Page 82; 157pp; English.
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                                                                          hypersensitive response
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Grobacterium vitis hypersensitivity response (HR) elicitor proteins associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (1.e. one in which intracellular bacterial growth and disease development do not cocur). Like other HR elicitors, the A. vitis elicitor intercoins in non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fund; bacteria or viruses; and to enhance growth, es, to increase yield or to provide carrier germination or maturation. The proteins can also be used to cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and elliminate the need for biological control agents or polluting
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0; Mismatches 116;
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P-PSDB; B11635, B11636, B11637, B11638.
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ID C75485 standard; cDNA; 565
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Matches 103; Conserv
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vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasctropic; antidabetic; hypotensive; dermatological; immunosuppressive; antidalamatory; antivaral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; ALDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coaqulation; thrombosis; contraceptive; ss.
                                               Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                     Human ORFX ORF1040 polynucleotide sequence SEQ ID NO:2079
 08-FEB-2001 (first entry)
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Homo sapiens

WO200058473-A2

05-0CT-2000

31-MAR-2000; 2000WO-US08621.

990S-0127636. 990S-0127728. 20000S-0540763. 99US-0127607 02-APR-1999; 05-APR-1999; 30-MAR-2000; 31-MAR-1999;

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2000-602362/57. P-PSDB; B41276.

Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease

Claim 5; Page 1566; 5507pp; English.

Sequence 565 BP; 122 A; 169 C; 148 G; 126 T; 0 other;

enhance coagulation; to inhibit thrombosis; and as a contraceptive

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                             Gaps
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0
 5.2%; Score 32.4; DB 21; Length 565; 50.6%; Pred. No. 0.95;
                             Indels
                            16;
                             0; Mismatches
                              78; Conservative
Query Match
Best Local Similarity
Matches 78; Conserv
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This genomic DNA sequence encodes insecticidal toxin protein Teah (see W17888-89) of Photorhabdus luminescens, a component of a toxin protein complex. Claimed toxins of P. luminescens (see W17811, w17884-89, W17899-900, W18301-06) can be produced by recombinant DNA methods and applied to, or genetically engineered into, insect larvae food and plants for insect control. The photorhabdus toxins are particularly effective against Southern corn rootworm, Colorado potato beetle, Western corn rootworm, meal worm, boll weevil and turf grub (Coleoptera), beet armyworm, black cutworm, cabbage looper, codling moth, corn earnyworm, black borer, tobacco hornworm and tobacco budworm (Lepidoptera), and are also active against insects of the orders Hymenoptera, piptera, Dictyoptera, Acarina and Homoptera. (All claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Photorhabdus sp. insecticidal protein toxins and DNA encoding them can be genetically engineered into insect larvae food and plants for insect control
caggicgagciggcgaaaagiggggggggggtttccigaaaggittacigaccaaictcgct 372
                                                                     432
                                                                                         96 GAAGGTAATGCGTTTGTAGGATTTGACCCCCAGTACCTGCTGGATGTGCCAGTGATGTGT 37
                       Insecticide; insect; toxin; pest control; biological control; Photorhabdus luminescens; TcaA; Southern corn rootworm; Colorado potato beetle; Western corn rootworm; meal worm; boll weavil; turf grub; Coleoptera; beet armyworm; black cutworm; cabbage looper; codling moth; corn earworm; European corn borer; tobacco hornworm; tobacco budworm; Lepidoptera; Hymenoptera; Diptera, Dictyoptera; Acarina; Homoptera; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fatig R;
Orr GL;
                                                                                                                                                                                                                                                                                                                                                                          Photorhabdus luminescens insect toxin protein TcaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blackburn MB, Bowen DJ, Ciche TA, Ensign JC, Ffrench-Constant RH, Guo L, Hey TD, Merlo DJ, Petell J, Roberts JL, Rocheleau TA, Schoonover Strickland JA;
                                                                                                                                            433 ggcactaccgcgcgctggggcattttgcgctga 466
                                                                                                                                                                               36 TTCACCTTCACGATCAGGGTCGGTTGCGAGGTAA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 38; Page 169-173; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                      T68841 standard; DNA; 3288 BP
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95US-0007255.
96US-0608423.
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                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Photorhabdus luminescens.
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28-FEB-1996;
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misc_difference 3641
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                                                                                                                                                               Query Match
Best Local Si
Matches 55;
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                                                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                                                                          2608 TCTTAATGCCGAAACCGGCGCTTAGCGCCCGCAGCACTTTCTGCTGTAACGCCGAATCCA 2549
                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                 tgggattgcgctgcttggcctgcatttgattatcgaaaaaatggcctggctgcatacgct 218
                                                                                                                              gattatggtgggcggtggcctgtatctctgctggatgggttaccagatgctacgtggtgc 278
                                                                                                                                                                         279 actgaaaaaagaggeggtttctgcacctgcgccacaggtcgagctggcgaaaagtgggcg 338
                                                           Gaps
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Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253015 to 254536, 254577 to 254615, and Y74253 to Y75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. 254537 to 254576 and 254616 to 255473 represent PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrheae ORF 589 partial DNA sequence SEQ ID NO:1827
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                                    Length 3288;
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Scalato E, S
                                                         Indels
                                                                                                                                                                                                                                     C; 768 G; 833 T; 0 other;
                                                                                                                                                                                                                       339 cagtttcctgaaaggtttactgaccaatctcgctaatccgaaag 382
                                  Score 32; DB 18; L
Pred. No. 3;
0; Mismatches 120;
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Ratti (
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, Pizza M, Rappuoli R,
 894 A; 793
                                  5.28;
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98US-0098994.
98US-0099062.
98US-0103749.
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                                                                                                                                                                                                                                                                                                      Z53939 standard; DNA; 2178
                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000 (first entry)
                                                         Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pizza M, I
Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria gonorrheae.
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P-PSDB; Y75177.
                                              Similarity
Sequence 3288 BP;
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
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09-OCT-1998;
09-OCT-1998;
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Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-11999
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                                  Query Match
Best Local S
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                                                                                                                                                                                                                                                                                 RESULT 10
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primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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specification, and is included to maintain the
base numbering given in the specification"
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0
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                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                           39;
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                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stealth virus nucleic acid clone, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.6; DE Pred. No. 3.4; 0; Mismatches
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tes 55; Conserv
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misc_difference 3751 /*tag= /note=	difference	misc_difference 3778 /*tag= /note=	misc_difference 3792 /*tag= /note=	misc_difference 3799 /*tag= /note=	misc_difference 3800 /*tag= /note=			difference	misc_difference 3819 /*tag= /note=		misc_difference 3841 misc_difference 3841 /*tag=	/note= misc_difference 3853 /*tag= /note=	misc_difference 3857 /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2760 SHNTBKGDYBKGDSDAHNTSYBDATASDANWAVSNSYTKGGNSBKGDDAWHTKVASNSYT 2701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2700 KGYCNWTSSYBSDASGNSNATBYSNGTYNCTSYDATYBSGSYDASSYBTCKARGDANVTT 2641
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                                                                                                                                                                        Indels
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                                                                                                                                             1. Similarity 13.4%; Score 31.6; DB 20; Similarity 13.4%; Pred. No. 5.1; 57; Conservative 176; Mismatches 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1989;
                                                                                                                                                 Local Si. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1990
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                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       006352
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                                                                                                                                                           Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccacggagcattattcagctcgacgatgtggtatcccaacatcgccgattggagcagcnn 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgccacaggtcgagctggcgaaaagtgggcgcagtttcctgaaaggtttactgaccaatc 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 ntacagaacttatgcagttgatatcataggtgatnnnaacnnnagtattcctgagaattt 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttatcgaaaaaatggcctggctgcatacgctgattatggtgggcggtggcctgtatctct 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 ttttggtcaaacacatgtgattgcaagcggcccagaggatgccccgccgcttgtattact 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 getggatgggttaccagatgctacgtggtgcactgaaaaaaagaggcggtttctgcacctg 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                            The DNA fragment encoding carboxyl esterase (CE) in B.subtilis Thai 18 (CBS 679.85) (Bell-HindIII fragment of 2kb originating from pNAPT-2 (see EP-233656)) was cloned into vector pT218R. Single-stranded DNA was prepared and subjected to oligonucleotide directed mutagenesis. Eleven different mutagenesis reactions were performed in order to substitute the 11 yaine residues of CE one at the time by a glutamine residue. The resulting mutant esterase was produced in E.coli DHI (ATCC 33849) and tested for stability in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presence of (S)-naproxen. The wild type enzyme is encoded by a DNA at least 70% homologous with this sequence (NNN-Lys in the wild type.) and is itself 70% homologous to the B. subtilis esterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                     Stabilised carboxyl esterase used for hydrolysis of S-naproxen obtd. by substituting or modifying basic residues of wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 903 BP; 227 A; 194 C; 191 G; 258 T; 33 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.2;
Pred. No. 3;
                                                                                                                                                Disclosure; Fig 1; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X53491 standard; DNA; 114955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate cancer; ss.
                 WPI; 1990-329202/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local_Similarity
Matches 105; Conserv
                                     P-PSDB; R07532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9913886-A1
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X53491;
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X53491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308
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The present sequence is that of open reading frame (ORF) mtbn6 (partial) of Mycobacterium tuberculosis. This is 1 of 8 ORFs (see 480135-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. The proteins encoded by these ORFs, i.e. Mysul-8 (see B19842-49) represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these WTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic
                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                                                                                                                                                               (PUBL-) PUBLIC HEALTH RES INST NEW YORK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 35pp; English
                                                                                                04-MAY-2000; 2000WO-US12257.
                                                                                                                                               99US-0132505
                                                                                                                                                                                                                                                                                             WPI; 2001-007153/01.
P-PSDB; B19847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccination methods
WO200066157-A1.
                                                                                                                                               04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09625519-A1
                                                 09-NOV-2000
                                                                                                                                                                                                                                                Gennaro ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T33535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T33535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes antisense oligonucleotides (X52869-X55271)
directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene
initiation codons, genomic flanking regions, intron-exon borders, the
initiation codons, genomic flanking regions, intron-exon borders, the
5'-end, the 3'-end and the juxta-section between coding and non-coding
regions and all segments of RNAs encoding proteins associated with one
or more diseases, conditions or mixtures. The antisense oligonucleotides
may be derived from sequences X5572-74. These multiple target
oligonucleotides (specifically X5180-271) can be used for the antisense
treatment of diseases and conditions. Typical diseases and conditions
are those associated with impaired respiration and inflammation,
allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
crespiratory distress syndrome, pain, cystic fibrosis, pulmonary
preferension, pulmonary vasoconstriction, employsema, chronic obstructive
pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
carcinomas e.g. colon cancer, breast cancer, lung cancer, pepatic
metastassized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                     New antisense oligonucleotides used in treatment of, e.g. \operatorname{pulmonary} vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 114955; 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis open reading frame mtbn6, partial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTBN6; tuberculosis; BCG; vaccine; infection; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 tttcttttttgtctctcagacc 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A89040 standard; DNA; 1536 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.0%;
                          98WO-US19419.
                                                                      98US-0093972.
                                                                                                                                               (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
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/*tag= a
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Conservative
                                                                                                                                                                                                                                              WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                       17-SEP-1998;
                                                                         09-JUN-1998;
                                                                                                17-SEP-1997;
                                                                                                                                                                                                 Nyce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A89040;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                             440 ccgcgcgctgggggcatttttgcgctgatcattgtcgaaacgctggcgtggtttaccgtcg 499
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCG delta 1; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.
                                                                                                   0;
                                                              Length 1536;
                                                                                                      Indels
Sequence 1536 BP; 224 A; 473 C; 519 G; 320 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
2327..11126
/*tote "BCG delta 1 deletion region"
/note= "BCG delta 1
                                                         5.0%; Score 30.8; DB 22; 58.9%; Pred. No. 5.2;
                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCG deletion region 1 and flanking sequences.
                                                                                                   0; Mismatches
                                                                                                                                                                                                                                500 ttgccagcctgtttgccctgccgcaaatgc 529
                                                                                                                                                                                                                                                        T33535 standard; DNA; 16885 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis strain BCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                              Query Match 5.0°
Best Local Similarity 58.9°
Matches 53; Conservative
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This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdeltal. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 other deletion regions (see T35353) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an virulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of the deletion; the deletions are detected either by detecting the presence or absence of deletion junctions (see T3358-46), or by checking the presence or absence of absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
                                                                                                                                                                                                                                            Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16885 BP; 3050 A; 5603 C; 5307 G; 2915 T; 10 other;
                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 66pp; English.
                                         96WO-US01938
                                                                                 95US-0390878
                                                                                                                        (PATH-) PATHOGENESIS CORP.
                                                                                                                                                                  Stover CK;
                                                                                                                                                                                                     WPI; 1996-393419/39.
                                                                                                                                                                Mahairas GG,
                                         15-FEB-1996;
                                                                              17-FEB-1995;
22-AUG-1996
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0 440 cogogogotogogoatttttgogotogatcattgtcgaaacgotggogtggtttaccgtcg 499 0; Gaps Query Match 5.0%; Score 30.8; DB 17; Length Best Local Similarity 58.9%; Pred. No. 17; Matches 53; Conservative 0; Mismatches 37; Indels q

DB 17; Length 16885;

500 ttgccagcctgtttgccctgccgcaaatgc 529 ò

7990 cggtcgcgcggatcgcgctgccgattc 8019

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Sequence 16, Application US/08390878

Patent No. 5706633

GENERAL INFORMATION:
APPLICANT: Maharins, Charles K.
APPLICANT: Mahairas, Gregory G.
ATITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 431;
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0.34;
US-08-996-685-7
US-08-989-478-1
US-08-980-179-2
US-08-880-179-2
US-08-880-179-1
US-08-980-179-1
US-08-96-842-2
US-09-096-847-2
US-09-096-867-2
US-08-096-623A-16
US-08-096-623A-17
US-08-096-623A-17
US-08-096-633A-17
US-08-866-633A-2
US-08-866-633A-2
US-08-866-633A-2
US-08-866-633A-2
US-08-866-633A-2
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US-08-453-323-1
US-08-440-520-1
US-08-257-9638-9
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Pred. No. 0.34
0; Mismatches
                                                                                                                                                                                                                                                                                      ALIGNMENTS
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; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-539
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Best Local Similarity 50.0
Matches 78; Conservative
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    RESULT 2
US-08-390-878-16
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                                                                                                6, 2001, 15:40:59 ; Search time 61.43 Seconds (without alignments) 1756.543 Million cell updates/sec
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Sequence 7
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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                                 Ltd.
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
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US-08-30-878-16

US-09-067-626-1

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US-09-067-626-3

US-09-010-928B-1

US-08-729-956-1

US-08-729-958-1

US-08-413-118-18

US-08-413-446-126

US-08-413-446-126

US-08-413-446-126

US-08-413-446-126

US-08-413-446-126

US-08-680-756A-51

US-08-680-756A-51

US-09-995-685-13

US-09-995-685-13

US-08-999-478-9

US-08-999-478-9

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US-08-999-478-9

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US-08-998-478-9

US-08-998-478-9
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                                                                        nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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length: 2000000000
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CLASSIFICATION:
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US-09-067-626-3
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Patent No. 6177086

GENERAL INFORMATION:
APPLICANT: Riley, Lee W.
APPLICANT: Riley, Lee W.
APPLICANT: Birt, Sabine
TITLE OF INVENTION: DNA MOLECULE CONFERRING ON MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS RESISTANCE AGAINST ANTIMICROBIAL REACTIVE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower, 20th STREET: Floor CITY: San Francisco
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEE-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15371A-17
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 10 FOR SEQ 1D NO: 16:
SEQUENCE CHRARATERISTICS:
FUNCTH: 16,875 base pairs
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COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 3.8;
0; Mismatches
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Best Local Similarity 58.9%;
Matches 53; Conservative C
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TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                  CITY: San Francisco
STATE: California
COUNTRY: USA
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STATE: New York
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GENERAL INFORMATION:
APPLICANT: Riley, Lee W.
APPLICANT: Riley, Lee W.
APPLICANT: BLY, Sabine
TITLE OF INVENTION: DNA MOLECULE CONFERRING ON MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS RESISTANCE AGAINST ANTIMICROBIAL REACTIVE
TITLE OF INVENTION: OXYGEN AND NITROGEN INTERMEDIATES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
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COUNTER LEADABLE FORM:

ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: DATEMIN Release #1.0, Version #1.30
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APPLICATION NUMBER: US 60/045,688
FILING DATE: 06-MN-1997
ATTORNEY AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,725
REFERENCE/DOCKET NUMBER: 19603/491
TELECOMMUNICATION INFORMATION:
TELEFAN: (716) 263-1304
TELEFAN: (716) 263-1304
TELEFAN: (716) 263-1304
TELEFAN: (716) 263-1206
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1244 base pairs
TYPE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,688
FILING DATE: 06-MAX-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09067626
Patent No. 6177086
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                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-09-067-626-1
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NAME/KEY:
LOCATION:
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US-08-279-996-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 tgattatcgaaaaatggoctggctgcatacgctgattatggtgggcggtggcctgtatc 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 tctgctggatgggttaccagatgctacgtggtgcactgaaaaaaagaggcggtttctgcac 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.9%; Score 30.2; DB 4; Length 1244;
Best Local Similarity 49.7%; Pred. No. 1.4;
Matches 77; Conservative 0; Mismatches 78; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boston, Rebecca S.
APPLICANT: O'Brian, Gregory R.
APPLICANT: O'Brian, Gregory R.
APPLICANT: O'Brian, Brocking A Ribosome Inactivating TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gibson
ADDRESSEE: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIA POSSING #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,651
FILING DATE: 19920908
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SIADIAY, KENNERD D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-199
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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REFERENCE/DOCKET NUMBER: 19603/491
TELECOMMONICACION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1304
INFORMATION FOR SEQ ID NO: 3:
SEQUIENCE CHARACTERISTICS:
LENGTH: 1244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charlotte
No. 5332808th Carolina
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/07941651
Patent No. 5332808
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TELEX: 575102
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1934 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-067-626-3
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CITY: CP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-07-941-651-1
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                                                                                                                                                                                                                                                                                                                             278 cactgaaaaaagagggggtttctgcacctgcgcccacaggtcgagctggcgaaaagtgggc 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1696 ACAGGATCTCGAAAGCCGTCTTCAGGTGGGCCGTCGACCCGACCGCTGAGATC 1748
                                                                                                                                                                                                                                                                                                                                                                                                                   338 gcagtttcctgaaaggtttactgaccaatctcgctaatccgaaagcgattatc 390
                                                                                                                                                4.7%; Score 29; DB 1; Length 1934;
48.0%; Pred. No. 4.6;
tive 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bass, Henry W.
APPLICANT: Bass, Henry W.
APPLICANT: O'Brian, Gregory R.
TITLE OF INVENTION: DNA Encoding A Ribosome Inactivating
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: ADDRESSE: Kenneth D. Sibley; Bell, Seltzer, Park and
ADDRESSEE: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,996
FILING BATE: 25-UUL-1994
CLASSIFICATION NUMBER: US/08/279,996
RICR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,651
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sibley/ Kenneth D.
REGISTRATION NUMBER: 31.665
REFERENCE/DOCKET NUMBER: 5051-199
TELEPHONE: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/08279996
; Patent No. 5552140
; GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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TELEX: 575102
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARATTERISTICS:
LENGTH: 1934 base pairs
                                                                                                                                         Query Match
Best Local Similarity 48.0%
watches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
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990..1826
                                                                990..1826
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                                        ; NAME/KEY;
; LOCATION:
US-07-941-651-1
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2166 GCTGGTGGACCCTACGGTCCAGGTGGTGCTGGACCCTACGGACCAGGTGGTGCTGGT 2225
                                                                                                                                                                               240 gtatctctgctggatgggttaccagatgctacgtggtgcactgaaaaaagaggcggtttc 299
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                                                                                                 180 gcatttgattatcgaaaaatggcctggctgcatacgctgattatggtggcggtggcct
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4.6%; Score 28.4; DB 1; Length 1038;
Best Local Similarity 50.0%; Pred. No. 5.2;
Matches 71; Conservative 0; Mismatches 71; Indels 0
                                                                                                                                                                                                                                                                                  300 tgcacctgcgccacaggtcgagctggcgaaaagtgggcgcagtttcctg 348
                                                                                                                                                                                                                                                                                                                                                                             US-08-680-726A-53
US-08-680-726A-53
Patent No. 5604197
EAREAL INFORMATION:
APPLICANT: Hearnes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN STATEM.
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-UL-1996
CLASSIFICATION: 424
ATTONREY/AGENT INFORMATION:
NAME: Connell, Gary J. 020
REGISTRATION NUMBER: 2618-46-C1
REGISTRATION NUMBER: 2618-46-C1
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-923
THYPE: NUCLEIC SECONDICTION:
SECONDENCE CHARACTERISTICS:
LENGTH: 1038 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Denver
STATE: Colora
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US-08-680-726A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                 0;
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                                                                                                                                   1636 TCAAGAAGCCGCAAGCGGTGACCATATCGGCGCTGGAGGGGAAGCAGGTGCAGAAATGGG 1695
                                                                                                                                                                                                                      278 cactgaaaaaaaaagaggcggtttctgcacctgcgccacaggtcgagctggcgaaaagtgggc 337
                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09010928B
Patent No. 5994099
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: HAYASH, Cheryl I
TITLE OF INVENTION: CODING THEREFOR
TITLE OF INVENTION: CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                1696 ACAGGATCTCGAAAGCCGTCTTCAGGTGGGCCGTCGACCCCGACCGCTGAGATC 1748
                                                                                                 0;
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                                                                                                                                                                                                                                                                                                 338 gcagittccigaaaggittacigaccaatcicgciaatccgaaagcgaitaic 390
                                                        Score 29; DB 1; Length 1934;
Pred. No. 4.6;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 2830;
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Pred. No. 5.7;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DUTA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
RECISTRATION NUMBER: 28977
REFERENCY/COCKET NUMBER: 1447-109P
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOLASCH & BIRCH
SUITE 500E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KC
STREET: 8110 GATEHOUSE RD. SU
CITY: FALLS CHURCH
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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                                                        4.78;
                                                      Query Match
Best Local Similarity 48.0
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.4
Matches 104; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-09-010-928B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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US-08-279-996-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 taatggtttggggctgggattgcgctgcttggcctgcatttgattatcgaaaaatggcct 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 GGTTATTCAAATTGAAAATGAAGTTTTTTATACTGATTTTATGGTTCAATTACCACGAGA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 TGATGAATTGGGATTAGTTTTAGCTGCCCCGCTCCATTTAATCAAGGTCAATATAGACG 476
477 GGTTATTCAAATTGAAAATGAAGTTTTTATACTGATTTTATGGTTCAATTACCACGAGA 536
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                                                                                                                                                                                    Sequence 53, Application US/09092409
Patent No. 6159478
GENERAL INFORMATION:
APPLICANT: Hand, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMETH RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATE.

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-0223
: INFORMATION FOR SEQ ID NO: 53:
contence CHARACTERISTICS:
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                                           266 tgctacgtggtgcactgaaaaa 287
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LENGTH: 1038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
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; LOCATION: 1..1
US-09-092-409-53
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US-08-413-118-18
Sequence 18, Application US/08413118
SEQUENCES OF TITLE OF INVENTION: CANINE HERESVIRUS GB, GC, AND GD AND USES THEREFOR UNMER OF SEQUENCES: 128
SUBSESPONDENCE ADDRESS:
                                                                                            APPLICANT: Pacietti, Enzo
APPLICANT: Limbach, Keith J.
TITLE OF INVENTION: UNCLEDINE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHALIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 840-333
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71;
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Pred. No. 5.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-220-151-18; Sequence 18, Application US/08220151; Patent No. 5529780; Patent INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 tgctacgtggtgcactgaaaaa 287
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.09
Matches 71; Conservative
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STRANDEDNESS: single
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; MOLECULE TYPE:
US-08-220-151-18
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APPLICATION NUMBER: US/08/473,446
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Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: CDNA
US-08-473-446-18
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US-08-473-446-18
Sequence 1B, Application US/08473446
Sequence 1B, Application US/08473446
GENERAL INFORMATION:
APPLICANT: DIMBACH, KEITH J.
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 ggctgcatacgctgattatggtgggcggtggcctgtatctctgctggatgggttaccaga 265
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                                                         ZIP: 10036

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE: 29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NEW YORK
ZOUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            CLASSITICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 30 MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELEPAN: (212) 840-333
FELEPAN: (212) 840-313
FELEPAN: (212) 840-312
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                    NEW YORK
: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 AACTIGITATITITIAAAGAA 758
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Best Local Similarity 50.09
Matches 71; Conservative
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US-08-413-118-18
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    NEW YORK
                                            COUNTRY:
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Patent No. 5688920
GENERAL INFORMATION:
APPLICANT: DAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: CANINE HERPESVIRUS GB, GC, AND GD AND USES THEREFOR NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 taatggtttggggttgggattgcgctgcttggcctgcatttgattatcgaaaaatggcct 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 GGTTATTCAAATTGAAAATGAAGTTTTTATACTGATTTTATGGTTCAATTACCACGAGA 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617 TGATGAATTGGGATTAGTTTTAGCTGCCCCCCCCTCCATTTAATCAAGGTCAATATAGACG 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%; Score 28.4; DB 3; Length 1320; 50.0%; Pred, No. 5.9; Live 0; Mismatches 71; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUPTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER REDABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CURTIS, MORRIS & SAFFORD,
STREET: 530 FIFTH AVENUE, 25TH FLOOR
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMEN, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
                                                                                                                                                                                          454310-2670
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29-MAR-1995
CLASSIFICATION:
PARTOR APPLICATION DATA:
PAPPLICATION NUMBER: 08/413,118
FILING DATE:
                                                                                               ATTOREY AGENT. INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION UNDBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INFORMATION:
TELEFAM: (212) 840-0712
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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Gaps

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5604 GGTTATTCAAATTGAAATGAAGTTTTTAAACTGATTTTATGGTTCAATTACCAGGAGA 5663
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                                                                                                                                                     146 taatggtttggggttgcgctgcttggcctgcatttgattatcgaaaaatggcct 205
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                                                               Score 28.4; DB 3; Length 1415;
Pred. No. 6.2;
0; Mismatches 71; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/08680726A
Patent No. 5804197
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Street, Suite 3500
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-UUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  836 AACTIGITATITITCTAAAGAA 857
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TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                 4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 10592 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                             Query Match
Best Local Similarity 50.vv
Rest Local 71; Conservative
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Best Local Similarity 50.0%
Matches 71; Conservative
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MEDIUM TYPE: Floppy
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US-08-680-726A-51
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US-08-680-726A-51
    US-08-473-446-126
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STATE:
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APPLICANT: LIMBACH, KETTH J.
TITLE OF INVENTION: UNCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
                                                                                                                                                                                                                                                                                                                                                                206 ggctgcatacgctgattatggtggggggtggcctgtatctctgctggatgggttaccaga 265
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                       ;0
                                                                                                                                                                                                                                                                            4.6%; Score 28.4; DB 1; Length 1415; 50.0%; Pred. No. 6.2; Live 0; Mismatches 71; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA
ZIE: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: CURTIS, MORRIS & SAFFORD, P.C. 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 454310-2670 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-333 TELEFAN: (212) 840-0712 INFORMATION FOR SEQ ID NO: 126: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/473,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 126, Application US/08473446
Patent No. 6017542
GENERAL INFORMATION:
...LEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 126: SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,118
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NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 50.09
Matches 71; Conservative
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FILING DATE:
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US-08-413-118-126
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Gaps

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Search completed: May 6, 2001, 16:25:06 Job time: 2647 sec

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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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em_gss_pln1; em_gss_pln2; em_gss_rod1; em_gss_rod2; em_gss_rod3; em_gss_rod3; em_gss_rod4; em_gss_rod4; em_gss_rod4; em_gss_rod4; em_gss_rod4; em_gss_rod4; em_gss_rod4; em_gss_rod4; em_gss_rod3; em_gss_rod4; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gss_rod3; em_gs_rod3; em		3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AL066784 Drosophil		AL076850 Drosophil	AL065826 Drosophil	AL059400 Drosophil	AL252739 Tetraodon	AL277501 Tetraodon	AL185829 Tetraodon	AL106392 Drosophil	BF621090 HVSMEa000	AL061710 Drosophil	AL108013 Drosophil	BE957648 601653724	AV720117 AV720117	AW721077 833011D11	BE196650 HVSMEh009	AQ438206 HS_5083_B
SUMMARIES	qI	CNS0073W	BE793235	CNS00JX7	CNS006RB	CNSOOCNG	CNS0300A	CNS04744	CNS028DO	CNS01671	BF621090	CNS0062R	CNS017GJ	BE957648	AV720117	AW721077	BE196650	AQ438206
	I ac	229	139	229	229	229	231	231	230	229	150	229	229	142	32	119	164	206
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æ	Query	9.5	0.0	5.8	5.8	5.8	5.7	5.7	5.7	5.7	5.6	5.6	5.6	5.5	5.5	5.4	5.4	5.4
	Score	38.6	36.2	35.8	35.6	35.6	35.2	35.2	35.2	35	34.6	34.6	34.4	34.2	33.8	33.6	33.6	33.4
	Result No.	7	1 m	4	c 2	0	c 2	80	σ	10	11	12	13	14	c 15	c 16	c 17	c 18

BASE COUNT 223 a 95 c 109 g 221 t 274 others  Ouery Match  Best Local Similarity 20.7%; Score 38.6; DB 229; Length 922;  Best Local Similarity 20.7%; Pred. No. 0.37;  Matches 47; Conservative 83; Mismatches 97; Indels 0; Gaps 0;  Qy 387 tatctactttggctcggtgtctcattgtttgtcggtgataacgttggcactaccgcgcg 446	RESULT 2 AQ280480/c LOCUS AQ280480 425 bp DNA GSS 22-NOV-1998 DEFINITION CITBI-E1-2516916.TF CITBI-E1 Homo sapiens genomic clone 2516816, DNA sequence.	ACCESSION AQ280480. VERSION AQ280480.1 GI:3906299 KEYWORDS KEYWORDS CSS. SOURCE ORGANISM Homeo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (Pases 1 to 425) AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and	Venter, J.C.  Venter, J.C.  TITLE Ves of a random human BAC End Sequence Database for Sequence-Ready Map Building JOURNAL Unpublished (1998)  COMMENT CASES: CITBL-E1-2516B16.TR  Contact: Mark Addams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200	Fax: 301 838 0208 Email: mdadams@tigr.org Clones available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends. Location/Qualifiers 1. 425 /organism="Homo sapiens" //Glone="taxon:9606" //Clone="2516816" //Clone="taxon:9606" //Clone="taxon:9606" //Clone="taxon:9606" //Clone="taxon:9606" //Clone="taxon:9606"	/cell_type="Form" /note="vycetor: pBeloBAC11; Site_1: BCORI; Site_2: ECORI; CalTech Human BAC Library D" CalTech Human BAC Library D" ORIGIN Query Match 6.2%; Score 38.4; DB 204; Length 425;
AW678 AW678 AW678 AQ550 AL066 BE284 AL065 AL065 AL066 AL132 BE459 BE459 BE459 BE459 BE459 BE459	. 2 4 6 3 3 4 6 6 1	CNSO073W 922 bp DNA GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit ALV66784 ALV66784 GSS.	Druschila melanogaster Druschila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Meotazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Meotara; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  1 (bases 1 to 922) Genoscope. Genoscope. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@denoscope.ens.fr	- Web: www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophia Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophia melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophia melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophia DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library	and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. 1. 922 1. 922 1. organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="bACR14D09"
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		3W TION TION ION N	ORGANISM DIO ORGANISM DIO DIA PEE MUS REFERENCE 1 AUTHORS GEN TITLE DIX JOURNAL SUB	COMMENT DEL	and full fou FEATURES source

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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BOGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Karutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                       CNSOOJX7 977 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC;
BACK39C01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
979 TATERGREGEGETCAGGCTTCTGGGTTGCCCTCCTGCTCCGGTGTTCCCTGTGT 920
                                                                                                                                    cttggcctgcatttgattatcgaaaaatggcctggctgcatacgctgattatggtgggc 231
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/db_xref="taxon:7227"
/clone_llb="RPCI-98"
/clone="BACR39C01"
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17.1%; Pred. No. 2.9;
Live 66; Mismatches
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Drosophila melanogaster
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Matches 22; Conservative
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/db_xref="texon.9606"
/db_xref="texon.9606"
/clone=_lib="NHL-MGC_7"
/clone=_lib="NHL-MGC_7"
/clssue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="nHl08 (phage-resistant)"
/lab_host="nHl08 (phage-resistant)"
/note="Organ: lung: Vector: pOTB7: Site_1: XhoI; Site_2:
FOCNI; cDNA made by oligo-dr priming. Directionally
cloned into EocNI/XhoI sites using the following 5'
adaptor: GGCAGGAG(5) Size=selected >500bp for average
insert size 1.8Bb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) 310 g 180 t IRT (Life Technologies)."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                 241 TGGGCTAGCCCAGGATCGGCTGGTGGGAGGTAGCTGCACTGGGGGGGATGTGAGGGGTT 182
                                                                                                                                                                                                                                 179 tgcatttgattatcgaaaaaatggcctggctgcatacgctgattatggtgggcggtggcc 238
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   Pred. No. 0.35;
); Mismatches 106; Indels
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Best Local Similarity 49.09
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Br 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial sogenic strain of Drosophila DNA provided by the BDGP from the isogenic strain y; cn bw sp, the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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AL252739.1 GI:7973751

GSS; qenome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
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Tetraodon nigroviridis genome survey sequence T7 end of clone
041G19 of library G from Tetraodon nigroviridis, genomic survey
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                     fruit fly.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="texon:\227"
/clone_lib="RPCI-98"
/clone="BACR26H16"
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When I wave genoscope.cors.it is presented out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BUGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI disestion of Drosophila DNA provided by the BDGP from the isogenic strain v3; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR26H16 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL059400
AL059400.1 GI:4946964
                                                                                               CNSO06RB 912 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14L21 of RPCI-98 library from Drosophila melanogaster (fruit
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI4L21"
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases ships sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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                                                                                    Rosst-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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Roset-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="086H24"
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/clone_lib="G"
/note="Genoscope sequence ID
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Best Local Similarity 54.7%;
Matches 70; Conservative (
                                                             (bases 1 to 1016)
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
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Vertebrata; Buteleostomi;

Butaryota; Metacad; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Burypterygii; Ctenosquamata; Acanthomorpha; Buacanthomorpha;

Bulypterygii; Acanthopterygii; Percomorpha;

Tetraodoniiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.

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Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
1 (bases 1 to 914)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouncau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                               Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                          2 (bases 1 to 914)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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/note="Genoscope sequence ID : COBG041AD10LP1-end : T7"
| 242 c 293 g 175 t 3 others
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                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Tetraodon nigroviridis genome survey sequence T7 end of clone
086H24 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
/clone="041G19"
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Pred. No. 4.3;
0; Mismatches
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1 Similarity 54.7%;
70; Conservative
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BF621090 835 bp mRNA EST 18-DEC-2000
HVSMEa0003P06f Hordeum vulgare seedling shoot EST library
HVCDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0003P06f,
mRNA sequence.
BF621090. GI:11884824
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Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y. Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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/clone="NSWEEGO03906f"
/clone=lib="Hordeum vulgare seedling shoot EST library
HVCDNA6001 (Cold stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
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229 c 158 g 216 t
                                                                                                                                                                                                                                                                                                       397 ggeteggtgtteteattgtttgteggtgataaegttggeaetaeeegegegettgggeatt 456
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Hordeum vulgare"
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High quality sequence start: 8
High quality sequence stop: 515.
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Pred. No.
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/clone="BACN15022"
/note="end : SP6"
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Wood,T.
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                                                                                                               Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracoon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracoon.
Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence SP6 end of BAC BAC BAC 15022 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/note="Genoscope sequence ID : C0AG244CF06SP1-end
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/plasmid="pselobacil"
/plasmid="taxon:7227"
/clone_lih="prossac"
                                                                                                                                                                                                                                                                                                                                                       /organism="Tetraodon nigroviridis"
/db_xref-"taxon:99883"
/clone="244L11"
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                                                                              aagaggcggtttctgcacctgcgccacaggtcgagctggcgaaaagtgggcgcagtttcc
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- Web : www.genoscope.cns. France (E mail : Sequeregenoscope.cns.)
- Web : www.genoscope.cns. France (E mail : Sequeregenoscope.cns.)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecoral digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                        CNSO062R 920 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR13J24 of RPCI-98 library from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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                 DB 150;
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               Score 34.6; DB
Pred. No. 6.5;
0; Mismatches
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/clone="BACR13J24"
/note="end : TET3"
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Best Local S:
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre C'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
CNSO17GJ 1101 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACNT/N18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL108013
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
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/clone="BACN17N18"
/note="end : SP6"
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/clone="LMAGE:383806"
/clone="LMAGE:383806"
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Eukaryota: Metacac: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metacac: Chordata; Catarrhini; Hominidae; Homo.

El (bases I to 832)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Oct 3, 2000 this sequence version replaced gi:10568353.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: CLONETECH Laboratories, Inc.
CONA Library Preparation: CLONETECH Laboratories, Inc.
CONA Library Preparation: CLONETECH Laboratories, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LALL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM525 row: p column: 05
High quality sequence stop: 2.

Location/Qualifiers

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4720117/C AV720117 501 bp mRNA EST 16-OCT-2000
LOCUS DEFINITION AV720117 GLC Homo sapiens cDNA clone GLCFEF09 5', mRNA sequence.
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tive 0; Mismatches 38; Indels 0;
DD 1058 ISYGYITGYGTGKCGCSTGKCTSTTGTGTGTGKSSBKKCGCTG 1101
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Best Local Similarity 60.09
Matches 57; Conservative
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Homo sapiens
Bullerayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 501)
Glan, B., WulT., Huang, Q., Huang, C., Rang, B., Gao, X., Xu, X., Xu, X., Lii, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zaon, L., Xu, S., Gu, M., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang
Homo sapiens CDNA GLC clones
Unpublished (2000)
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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Chinese National Human Genome Center at Shanghai
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GenCore version 4.5
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OM protein - protein search, using sw model

6, 2001, 14:38:48; search time 34.23 Seconds (without alignments) 344.015 Million cell updates/sec Мау Run on:

Title: Perfect score: Sequence:

US-09-466-935-4 1054 1 MIMIELTYVAMVHIVALMSPG......IDGFAGALFAGFGIHLIISR 206

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

390729 Total number of hits satisfying chosen parameters:

390729 seqs, 57163235 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A. Selicsey\_dul:\*

SIDSZ/gcgdata/geneseq/geneseqp\_AA1981.DAT:\*

SIDSZ/gcgdata/geneseq/geneseqp\_AA1991.DAT:\*

\_Geneseq\_0401:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
No.	Score Match Length DB I	Match	Length	DB	ID	Description
1 1	1054	100.0	206	21	X99598	E. coli L-threonin
7	261.5	24.8		21	B01786	Escherichia coli Y
3	190	18.0		21	B01787	Escherichia coli Y
4	179.5	17.0		21	B11637	A. vitis hypersens
5	122	11.6		21	X99597	E. coli L-homoseri
9	122	11.6		21	Y79298	E. coli RhtB prote
7	105	10.0	236	18	W37715	C. dlutamicum Lys
80	103	9.6		21	B01789	Escherichia coli Y
6	101	9.6		21	B01788	Escherichia coli Y
10	94.5	9.0		21	B40407	Human ORFX ORF171
11	91	8.6		17	R87527	Mel-linked mlgA de

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112 114 116	19 20 22 23	422222	20 20 20 20 20 20 20 20 20 20 20 20 20 2	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

Tokhmakova IL; Livshits VA, Zakataeva NP, Aleshin VV, Belareva AV, L-threonine resistance; L-threonine synthesis; rhtC; L-homoserine; L-valine; L-leucine. E. coli L-threonine resistance protein, RhtC. ¥. Y99598 standard; Protein; 206 99EP-0125406. 98RU-0123511 (first entry) (AJIN ) AJINOMOTO KK. WPI; 2000-414602/36. N-PSDB; A48443. Escherichia coli. 23-DEC-1998; EP1013765-A1 20-DEC-1999; 08-SEP-2000 28-JUN-2000 Y99598; RESULT Y99598 

Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -

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EP1016710-A2.
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                                                                                                   Sequence
                                                                                                                               Query Match
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Matches
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                The present sequence is the L-threonine resistance protein, RhtB, from Escherichia coli. The coding sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing L-threonine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-homoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion protein \cdot
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                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                       E. coli; yahN gene; amino acid production; excretion protein gene; amino acid excretion protein.
                                                                                                                                                                                                                                                                                                      1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGL
                                                                                                                                                                                                                                                                 121 TNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGY
                                                                                                                                                                                          ;
0
                                                                                                                                                                      Length 206;
                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli YahN amino acid excretion protein.
                                                                                                                                                                    100.0%; Score 1054; DB 21;
100.0%; Pred. No. 1.9e-112;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                              QRLAKWIDGFAGALFAGFGIHLIISR 206
1; Page 15-16; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                       B01786 standard; Protein; 223
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99RU-0104431
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 206; Conservative
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N-PSDB; A52688.
                                                                                                                                         206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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Tokhmakova IL;
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                                                                                                                                         Sequence
Claim
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                                      The present sequence is the YahN amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of it gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 itqceeifslirivggayllwfawcsmr----rqstpqmstlqqpisapwyvffrr 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRS-----FLK 117
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid production; excretion protein gene;
                                                                                                                                                                                                                                                                                                                                                                                                      4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI
                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                     Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli Yeas amino acid excretion protein.
                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                   24.8%; Score 261.5; DB 21; 28.2%; Pred. No. 6.5e-22; ive 50; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGYQRLAKWIDGFAGALFAGFGIHLI 203
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Claim 1; Page 19; 29pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B01787 standard; Protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. coli; yeas gene; amino acamino acid excretion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99EP-0125263.
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99RU-0104431.
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                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 58; Conserv
                                                                                                                                                                                                                           223 AA;
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Tokhmakova IL;
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Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, alamine, valine, histidine, isolaucine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences B11630-B11688 represent proteins from Agrobacterium vitis which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (A61501-A61524) encoding the A. vitis HR elicitor proteins. The HR is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
                                                                                                                                                                                                                                     128 AIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAW------FTVVASLFALPQMRRGY 180
                                                                                                                                                                                                                                                                                    68 AWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPK 127
                                                                                                                                                  Gaps
                                                                                                                                                                                       --- VMVWAGIALLGLHLIIEKM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant.
                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. vitis hypersensitive response elicitor protein, SEQ ID NO:9.
                                                                                                                         Length 212;
                                                                                                                                                Indels
                                                                                                                         Score 190; DB 21;
Pred. No. 8.8e-14;
                                                                                                                                                                        13 IVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG--
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 85-86; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     B11637 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang H;
                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                    181 QRLAKWIDGFAGALFAGFGIHL 202
                                                                                                                                                                                                                                                                                                                                   (CORR ) CORNELL RES FOUND INC.
                                                                                                                       18.0%;
28.2%;
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                                                                                                                                                57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobacterium vitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-376567/32.
                                                                                                                                      Local Similarity
                                                                                    212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200028056-A2
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                                                                                       Sequence
                                                                                                                          Query Match
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occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents or polluting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tokhmakova IL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 KMAWLHTLIMVGGGLYLCWMGYQMLRGALKK----EAVSAPAPQVELAKSGRSFLKGLLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLIIE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| : :||| || || : : || : :||
25 lliasitwlavlspgadfamvsrnsflygrksglaasmgiaiacwfhviyamfgiaiigh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Belareva AV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-homoserine resistance; L-homoserine synthesis; rhtB; L-threonine; L-valine; L-leucine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5e-12;
95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. coli L-homoserine resistance protein, RhtB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 179.5;
Pred. No. 1.5
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nes 54; Conservative
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N-PSDB; A48442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local S
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                                                                                                                                                                                                                                                                                                                 æ
                                                                                    The present sequence is the L-homoserine resistance protein, RhtB, from Escharichia coli. The coding sequence may be used to impart L-homoserine resistance on E. coli bacteria, which would be useful for producing a high yield of L-homoserine L-homoserine resistance means that the bacteria will be able to grow on a minimal medium containing L-homoserine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-homoserine, which accumulates. The accumulated amino acids can then be removed from the culture medium. The bacterium of the present invention may also be used to synthesise L-threonine, L-valine and L-leucine at increased levels.
            Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                117 KGLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQM 176
                                                                                                                                                                                                                                                                                                                                                                                             61 HLII--EKMAWLHTLIMVGGGLYLCWMGYQMLR--GALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                                                                                                                                                                                                                                                                                                                                       66 rsviafevlkw-----agaayliwlgiqqwraagaidlkslastgsrrhl-----fg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                            ----MVWAGIALLGL 60
                                                                                                                                                                                                                                                                                                                                                                    11 ltsiiltlspgsgaintmttslnhgypag----gvycwasdrtgdsycagwrgvgtlfs 65
                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homoserine resistance, RhtB protein; L-homoserine; L-alanine; L-isoleucine; L-valine; L-threonine,
                                                                                                                                                                                                                                                                                       Length 205;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Belareova AV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli RhtB protein imparting homoserine resistance.
                                                                                                                                                                                                                                                                                                                 :68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|||| | :|
|165 atlagrialwikgpkqmkalnkifgslfmlvgallasar 203
                                                                                                                                                                                                                                                                                       Score 122; DB 21;
Pred. No. 4.9e-06;
36; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                           10 MVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 RRGYQRLAKWIDG------FAGALFAGFGIHLIISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aleoshin VV,
                          to enhanced RhtC protein activity, us
L-homoserine, L-valine and L-leucine
                                                               2; Page 13-14; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y79298 standard; Protein; 205 AA
                                                                                                                                                                                                                                                                                       11.6%;
21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-0118581
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                                                                                                                                                                                                                                                                                                   Local Similarity 21.09
nes 46; Conservative
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N-PSDB; 294405.
                                                                                                                                                                                                                                                  205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Livshits VA,
Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2000
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                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                         Query Match
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                                                                Claim
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Matches
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Novel RhtB protein, useful for generation of L-homoserine resistance in Escherichta bacteria and large-scale production of e.g. L-homoserine and L-alanine
                                                                                                                                                            protein, RhtB, which participates in resistance to L-homoserine.

Amplification of the rhtB gene (see 294405) results in an improvement of the amino acid productivity of E. coll. The invention provides: a protein comprovising the present sequence or including a deletion, substitution, insertion and/or addition of 1 or more amino acids and having the activity of making a bacterium resistant to L-homoserine; DNA encoding RhtB; a bacterium, especially of the genus Escherichia, in which L-homoserine cresistance is enhanced by amplifying the copy number or increasing the expression rate of the rhtB DNA, the DNA being carried on a multicopy vector or on a transposon; and a method for producing an amino acid by cultivating the bacterium in a culture medium to produce and accumulate the amino acid in the medium, from which it is recovered. The method is used for the production of L-homoserine, L-alanine, L-isoleucine, L-valine or L-threonine (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysG; LysE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HLII--EKMAWLHTLIMVGGGLYLCWMGYQMLR--GALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 rsviafevlkw-----agaayliwlgiqqwraagaidlkslastqsrrhl-----fg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --tivvdiivmigy 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 MYHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGV------MVWAGIALLGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |: :|||
11 ltsiiltlspgsgaintmttsInhgypag-----gvycwasdrtgdsycagwrgvgtlfs
                                                                                                                                            present sequence is that of the novel Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. glutamicum Lys E protein (lysine export protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , DB 21;
4.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 RRGYQRLAKWIDG------FAGALFAGFGIHLIISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 122; DB 21.0%; Pred. No. 4.9e.ive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                  Claim 1; Page 11-12; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 21.09
nes 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-1997
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AA.
                                                                                                                                                                       Claim 1; Page 25; 29pp; English.
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            99RU-0104431,
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99RU-0104431.
98RU-0124016.
                                                        Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                  (AJIN ) AJINOMOTO CO INC.
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                                                                                                                           production of increasing the
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175 rtakaqriinlvvg 188
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                                                                                         WPI; 2000-414802/36.
N-PSDB; A52691.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             211 AA;
                                                                    Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1016710-A2
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09-MAR-1999;
30-DEC-1998;
            09-MAR-1999;
                                                        Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-2001
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                                                                                                                            Increased
                                                                                                                                        comprises
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                    protein
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                                                                                                                                             This sequence is the LysE protein product, a lysine export protein. LysG and LysE encode a lysine transport regulatory protein and an export protein. Its protein. Its protein in a microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, confinents and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                            60 vdllsnaapivldimrw----ggiayllwfavmaakdamtnk---veapqiieetep 109
                                                                                                                                                                                                                                                                                                                                                                                                         LHL------IIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQV----- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tvpddtplggsavatdtrnrvrvevsvdkgrvwvkpmlmaivltwlnpnayldafvfigg 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 VFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGAL 194
                                                                                                                                                                                                                                                                                                                                                                          1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVWVWAGIA-LLG 59
                                                                 Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli, yggA gene, amino acid production; excretion protein gene; amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ELAKSGRS--------FLKGLLTNLANPK----AIIYFGS
                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli YggA amino acid excretion protein.
                                                                                                                                                                                                                                                                                                             Score 105; DB 18;
Pred. No. 0.00051;
5; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B01789 standard; Protein; 211 AA.
                                                                                                                           Claim 42; Page 10; 16pp; German.
                                                                                                                                                                                                                                                                                                                                      36;
           Vrlijc M;
                                                                                                                                                                                                                                                                                                             10.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                      51; Conservative
           Sahm H,
                                  WPI; 1997-333867/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 FAGFGIHLII 204
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                             N-PSDB; T96816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33-JAN-2001
           Eggeling L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35-JUL-2000
                                                                                                                                                                                                                                                                               Sequence
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The present sequence is the YggA amino acid excretion protein from Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                          of L-amino acids by an Escherichia bacterium
the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 A----NPKAIIYFGSVFSLFVGDNVGTTARWGIFAL-IIVETLAWFTVVASLFA--LPQM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRCALKKEAVSAPAPQVELAKSGRSFLKGLLTNL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI 63
Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. coli; yfiK gene; amino acid production; excretion protein gene;
amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
Nakanishi K, Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli YfiK amino acid excretion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 103; DB 21; ilarity 27.8%; Pred. No. 0.00075; Conservative 25; Mismatches 93;
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7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame, ORFX; detection; cytostatic; hepatotropic; vulnetary; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; antionvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidialmamatory; antival; antibacterial; antifungal; antifungal; antifungal; antimosuppressive; antinifanmatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoinmune disorder; astima; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                         Escherichia coli. This protein is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in threonine, histidine, glutamic acid and proline is achieved if multiple copies of its gene are transfected into a bacterium. The bacterium used
                                                                                                                                 Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 LLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ---fslavidpaavh-llswagaayivwlawkiatsptkedg1ga------kpisfw 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG----VMVWAGIA 56
               Zakataeva NP, Nakanishi K, Aleshin VV, Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is the YfiK amino acid excretion protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%; Score 101; DB 21; Length 195; 22.0%; Pred. No. 0.0012; tive 32; Mismatches 72; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX ORF171 polypeptide sequence SEQ ID NO:342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B40407 standard; Protein; 130 AA
                                                                                                                                                                                                                 Claim 1; Page 23; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Conservative
                                                                     WPI; 2000-414802/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      195 AA;
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                                                                                            N-PSDB; A52690
                                  Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                 coli.
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Best Local S:
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                        protein
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B40407
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represent the human ORRY open reading frames 1 to 3161. The ORRY sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; cardiant; thrombolytic; cardiant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; cardiviral; antithrough; antiinflammatory; antibacterial; antiviral; antithremmatic; antithroid; and antianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORRY-associated disorder. The nucleic acids can be used to express ORRX or proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID) AIDS, viral, bacterial or fungal infection, malaria, autoimmune discuences, nocturnal haemoglobinuria, antiinflammatory disease; cenhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 YLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 yllylayatwrd--rsafamndtptvatars--lilrgfilnilnpkltifflaflpqfv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C74446 to C77606 encode the proteins given in B40237 to B43397,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marine melA; selectable marker; oyster larva settlement; pigmentation; melanin; p-hydroxyphenylpyruvate-hydroxylase; mlgA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.0%; Score 94.5; DB 21; 25.7%; Pred. No. 0.0038; ative 22; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 608; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R87527 standard; Protein; 153 AA.
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                                                             02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                              99US-0127607
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                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
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Les 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; C74616.
                                                                                                                                                                                                                                                                                     Shimkets RA,
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Sequence
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Best Local
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                           R98004;
                                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                   Matches
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δy
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                                                                                                                                                                                                                                                                                                                                    99 MLRGALKKEAVSAPAPQVELAKSGRSFL-KGLLTNLANPKAIIYFGSVFSLFVGDNVGTT 147
                                                                                                                                                                                                                                                                                                                                                                   43 LGITCGV--MVW-----AGIAL-----LGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marine bacterium; melanin synthesis; marine exopolysaccharide;
                                                                                                                                                            Novel gene encoding marine melA from Shewanella - useful as selectable marker in genetic engineering and for inducing larval
                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                     The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colwelliana melA gene (T06766), and was designated mlgA (mel-linked gene). The role of the encoded protein (R87527) was unclear as deletion subcloning in E. coli demonstrated that only melA was required for melanogenesis.
                                                                                                                                                                                                                                                                                          8.6%; Score 91; DB 17; Length 153;
25.5%; Pred. No. 0.012;
ive 31; Mismatches 54; Indels
       Shewanella colwelliana strain LSTDYF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. colwelliana MlgA protein sequence.
                                                                                                                                                                                            Example 7; Fig 14; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                     (UYMA-) UNIV MARYLAND BALTIMORE.
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pglmvllsiimmt-effsmla 142
                                                                                                                                                                                                                                                                                                                                                                                           148 ARWGIFALIIVETLAWFTVVA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                  W73358 standard; Protein; 153
                                                                     93US-0148945.
90US-0496804.
92US-0974837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mlgå; marine bacterıum; mere
UV blocker; sunscreen; MelA.
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                                                      90US-0496804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shewanella colwelliana
                                                                                                                     Weiner RM;
                                                                                                                                    WPI; 1996-039515/04.
N-PSDB; T06767.
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                    153 AA;
                                                                                                                                                                             oyster settlement
                                                                     08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                      21-MAR-1990;
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                      US5474933-A
                                       12-DEC-1995
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                                                                                                                     Fugua WC,
                                                                                                                                                                                                                                                                    Sequence
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This sequence is the Shewanella colwelliana MigA protein, which is related to the MelA protien of the invention. The invention relates to MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides. The MelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass or in paints and coatings for plastics, synthetic resins and fabrics, rubber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 MLRGALKKEAVSAPAPQVELAKSGRSFL-KGLLTNLANPKAIIYFGSVFSLFVGDNVGTT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MelA melanin protein from marine bacteria - useful as UV blocker in e.g. cosmetics % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} 
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                                                                                                                                                                                                                                              /note= "immunogenic peptide 1004, claim 11 page 19" 418..431
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125..138
/label= 1003
/note= "inmunogenic peptide 1003,
252..265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oestrogen-regulated gene; pLIV1; breast cancer;
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Local Similarity 25.5%; Pred. No. 0.012;
Les 36; Conservative 31; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oestrogen-regulated pLIV1 gene-encoded protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV MARYLAND BALTIMORE.
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95US-0476254.
90US-0496804.
92US-0974837.
93US-0148945.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-058995/05.
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07-JUN-1995;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                                                                                                                                                                    08-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 agvatl----aw---mvimgdglhnfsdglai--gaafteglssglstsvavfch 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 PAPQ-----VELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 IVETLAWFTVVASLFALPQM-----RRGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                                                                                                                                                                                                                                                                                                                                                                                     The polypeptide (R98004) encoded by a partial cDNA clone regions, 1003, 1004 and 1005, that were used to raise polyclonal antibodies in rabbits. Peptides 1004 and 1005 were most immunogenic, generating ELISA-positive sera at dilutions of 1/200000. Cross-reactivity studies using the 3 peptides inchanges reactivity studies using the 3 peptides identified 7 positive specific sera in tumnour samples from 74 patients with primary breast cancer. The pLIVI polypeptide was expressed in the cytosol of cestrogen receptor-positive epithelial cells of breast tumnours. Its presence can be used to predict the propensity for metastatic spread or the responsiveness of a breast tumnour to metastatic spread or the responsiveness of a breast tumnour to treating breast cancer and metastation may be used as a means of treating breast cancer and metastasis.
                                                                                                                                                                                                                                                                                                                                         Oestrogen-regulated pLIV1 gene and deduced polypeptide - useful for predicting the propensity for metastatic spread or the responsiveness to endocrine treatment of breast tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 431;
/label= 1105
/note= "immunogenic peptide 1005, claim 11
page 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 AGIALLGLHLIJEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by pLIV1 gene partial sequence.
                                                                                                                                                                                                                                        Green CD, Manning DL, Nicholson RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.5; DB Pred. No. 0.14; L; Mismatches
                                                                                                                                                                                                         (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 14-16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.2%; Scor
27.4%; Pred
ative 21; P
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                                                                                                                                     94CA-2132500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                         WPI; 1996-268987/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 AA;
                                                                                                                                                                                                                                                                                          N-PSDB; T33219;
N-PSDB; T33220.
                                                                                                                                     20-SEP-1994;
                                                                     CA2132500-A
                                                                                                      21-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                          See JM,
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This sequence is encoded by a partial sequence of the pLIV1 gene. This protein sequence is an oestrogen regulated gene associated with breast cancer. This sequence can be used in the method of the invention. The method is for determining the risk of metastasis of a female breast tunnour and predicting the responsiveness of a female breast tunnour compresses a polypeptide comprising at least 14 continuous amino acids of the protein encoded by this sequence. The method is useful for determining the risk of metastasis of a female breast tunnour and to predict the responsive of the female breast tunnour and to pilVI expression is highly predictive of tunnour to hormone treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 PAPQ-----VELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 agvatl------aw---mvimgdglhnfsdglai--gaafteglssglstsvavfch 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 AGIALLGLHLIIEKMAWIHTLIMVGGLYLCWMGYQMLRGALKKEAVSA------ 101
                                                                                                                                                                                                                                                            Assessment of metastatic risk or oestrogen responsive-ness in breast cancer - by detecting expression of pLIV1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 IVETLAWFTVVASLFALPQM ------RRGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.2%; Score 86.5; DB 19;
Best Local Similarity 27.4%; Pred. No. 0.14;
Matches 49; Conservative 21; Mismatches 56;
                                                                                                                                                                                    Green CD, Manning DL, Nicholson RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloramphenicol resistance; mutagenesis
                                                                                                                                                         (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloramphenicol resistance gene prod.
                                                                                                                                                                                                                                                                                                       Claim 1; Column 5-10; 11pp; English.
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                                                                                                                             94US-0311023
                                                                                                  94US-0311023
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                                                                                                                                                                                                               WPI; 1998-031740/03.
N-PSDB; T99070, T99071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 AA;
              Homo sapiens
                                                                                                  22-SEP-1994;
                                                                                                                             22-SEP-1994;
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                                         US5693465-A.
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qq
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8.2%; Score 86; DB 11; Length 390;
Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 47; Conservative 35; Mismatches 78; Indels 68; Gaps:
                                                                                                                                                                                                                                                                                                                                                                               94 LKKEAVSAPAPQVELAKSGRSFLKGLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 VL--GITCGVMVWAGI---ALLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGA--- 93
                                                                                                                                                                                                                             When expressed in host cells this confers Chloramphenicol resistance on them.
                                                                                                                                                                                                                                                                                                                                                                1 MIMI,FLTVAMVHIVALMSPGPDFFFVSQ....-.--TAVSRSRKEAMMG 41
                                                                                                                                              Site specific mutagenesis of DNA at restriction enzyme positions by treating corresp. restriction fragments with hydroxylamine, and new mutated sequences and transformed microorganisms
                                                              Kassing F, Kalinowski J, Arnold W, Winterfeldt A, Puhler A;
Kautz P-S, Thierbach G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 ALIIVETL----AWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1988; 88DE-3841454.
                                                                                                                                                                                                  Disclosure; ; p; German.
                                                                                                     WPI; 1990-186465/25.
NPSDB; Q04775.
                                      (DEGS ) DEGUSSA AG.
                                                                                                                                                                                                                                                                      390 AA;
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Search completed: May 6, 2001, 14:38:49 Job time: 395 sec

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89 MLRGALKKEAVSAPAPQVELAKSGRSFL-KGLLTNLANPKAIIYFGSVFSLFVGDNVGTT 147
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                       Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Seduence Sed
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-UUN-1995
CLASSIFICATION: WINSTER: US/08/476,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: WATSON COLE STEVENS DAVIS, P.L.L.C.
STREET: 1400 K STREET NW
CITY: WASHINGTON
             US-08-176-873-2
US-08-477-451-12
US-08-805-118-3
US-08-724-394A-9
US-08-852-824-4
US-08-356-060A-34
US-08-356-060A-34
US-08-118-270-43
PCT-US93-06528-43
US-08-128-186-5
US-08-528-18-5
US-08-528-18-5
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US-09-231-227-2
US-07-816-283-2
US-07-816-283-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, JAMES A.
REGISTRATION NUMBER: 31,714
REFERENCE/POCKET NUMBER: JAP30319C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-0038
TELEFAX: 202 628-0038
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WEINER, RONALD M.
APPLICANT: FOUGH, WILLIAM C.
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08476254 Patent No. 5846531 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // MOLECULE TYPE: protein US-08-476-254-7
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                                                                                                                                                         May 6, 2001, 14:39:23; Search time 21.59 Seconds (without alignments) 183.300 Million cell updates/sec
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                                                                                                                                                                                                                                                                US-09-466-935-4
1054
1 MLMLFLTVAMVHIVALMSPG......IDGFAGALFAGFGIHLIISR 206
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Seguence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                       GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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102 PAPQ-----VELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALI 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 ----RPGALSALGAIAPPLAA---GAAFSALVLDRPLPS---GLFLGIVLSVTAVSVIAK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 IVETLAWFTVVASLFALPOM------RRGYQRLAKWIDGFAGALFAGFGIHLII 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molor, James
APPLICANT: Molor, Istvan
APPLICANT: Work Molor
APPLICANT: Gorlach, Joern
APPLICANT: Gorlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILIO DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.2%; Score 86.5; DB 1; Length 431; Best Local Similarity 27.4%; Pred. No. 0.085; Matches 49; Conservative 21; Mismatches 56; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.8%; Score 82; DB 4; Length 713; Best Local Similarity 22.0%; Pred. No. 0.55; Matches 46; Conservative 29; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AGIALLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSA---
REGISTRATION NUMBER: Reg. NO. 5693465 32,925 REFERENCE/DOCKET NUMBER: WCM.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
                             REFERENCE/DOCKET NUMBER: WC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/521-2297
TELEFAX: 703/685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Sorangium cellulosum US-09-335-409-11
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
                                                                                                                            TELEFAX: 703/685-0573
TELEX: 248425
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-311-023-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 SLFALPOMRRGY---
                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                     TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-09-335-409-11
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43 LGITCGV--MVW-----AGIAL-----LGLHLIIEKMAWLHTLIMVGGCLYLCWMGYQ 88
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APPLICANT: GEE, JULIA MATGATECT
APPLICANT: GREE, JULIA MATGATECT
APPLICANT: GREEN, Christopher Douglas
TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: BREAST TUMOURS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.6%; Score 91; DB 6; Length 153
25.5%; Pred. No. 0.0064;
tive 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: TBM PC COMPATIBLE
COMPATER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25 (EPO)
SOFTWARE: PATENTON DATA:
APPLICATION NUMBER: US/08/311,023
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
                                                                                                                                                                                                                                          RESULT 2
5474933-4
; Patent No. 5474933
; PAPPLICANT: EINER, RONALD M.; FUQUA JR., WILLIAM C.
TITLE OF INVENTION: MARINE MELA GENE
NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
HILNG DATE: 08-NOV-1993
; PRIOR APPLICATION NUMBER: 974,837
FILING DATE: 10-NOV-1992
; APPLICATION NUMBER: 974,837
FILING DATE: 10-NOV-1992
; APPLICATION NUMBER: 974,837
FILING DATE: 11-NOV-1993
; FILING DATE: 21-MAR-1990
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Patent No. 5693465
GENERAL INFORMATION:
GAPPLICANT: MANNING, David Lockwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Young & Thompson 745 South 23rd Street
                                                                                                                                           123 PQLMVLLSIIMMT-EFFSMLA 142
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                                                                                           148 ARWGIFALIIVETLAWFTVVA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 ARWGIFALIIVETLAWFTVVA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.5%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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34 SRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTL--IMVGGGLYLCWMGYQMLR 91
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
TELEPAX: 317-277-1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 1307 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 18.4%,
watches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE:
US-08-395-246C-2
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                                                                                                                                                                                                                                                                                                    US-08-395-246C-2
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                                                                                                                  Sequence 3, Application US/09097759A

Patent No. 5972663

GENERAL INFORMATION:
APPLICANT: Winterhalter Mr., Christopher
APPLICANT: Leinfelder Mr., Walfred
TITLE OF INVENTION: Macroorganisms and Processes for the Fermentative
TITLE OF INVENTION: Preparation of 1-cysteine,
TITLE OF INVENTION: Loysteine, N-acetylserine or Thiazolidine Derivatives
TITLE OF INVENTION: Loysteine, N-acetylserine or Thiazolidine Derivatives
TITLE OF INVENTION INDER: US/09/097,759A
CURRENT APPLICATION NUMBER: US/09/097,759A

CURRENT FILING DATE: 1998-06-16

EARLIER FILING DATE: 1997-06-19

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 299

TYPE: PRT
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APPLICANT: Winterhalter Mr., Walfred
APPLICANT: Leinfelder Mr., Walfred
TITLE OF INVENTION: Microorganisms and Processes for the Fermentative
TITLE OF INVENTION: Deparation of Li-cysteine,
TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives
TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives
TITLE OF INVENTION: L-cysteine, N-acetylserine or Thiazolidine Derivatives
CURRENT APPLICATION NUMBER: US/09/097,759A
CURRENT FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: DE 197 26 083
EARLIER TILING DATE: 1997-06-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 GALKKEAVSAPA-----PQVELAKSGRSFLKGL-LTNLANPKAIIYFGSVFSLFVGDNV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 SRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTL--IMVGGGLYLCWMGYQMLR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 --LRFMLVAFPAIFFVARPKVPL-----NLLLGYGLT-----ISFAQFAFLFCAINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 80.5; DB 2; Length 299; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.6%; Score 80.5; Di
Best Local Similarity 25.0%; Pred. No. 0.25,
Matches 45; Conservative 27; Mismatches
  Sequence 2, Application US/09097759A Patent No. 5972663 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Escherichia coli
US-09-097-759-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Escherichia coli
US-09-097-759-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 45; Conserv
                                                                                      RESULT 5
US-09-097-759-3
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US-09-097-759-2
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LENGTH: 306
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                                                                                                                                                                                              GMPAG---LASLVLQAQAFFTIMLGAFTFGBRLHGKQ------LAGIALAIFGVLVLI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 ---WMGYOML, RGALKK -----EAVSA ------PAPQVELAKSGRSFLK 117
                                                                                                                                                                   GTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLII 204
                                                                     92 GALKKEAVSAPA-----PQVELAKSGRSFLKGL-LTNLANPKAIIYFGSVFSLFVGDNV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 -----MMGVLGITCGVMVWAG---IALLGLHLIIEKMAWLHTLIWVGG--GLYLC-- 83
45 -- LRFMLVAFPAIFFVARPKVPL----NLLLGYGLT-----ISFAQFAFLFCAINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Peery, Robert B.
APPLICANT: Skaftud, Paul L.
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: ASPERGILLUS FLAVUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 GLLTN---LANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC_compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%; Score 79.5; D
18.4%; Pred. No. 2.4;
tive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,246C
FILING DATE:
                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08395246C Patent No. 5773214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Eli Lilly and Compa
STREET: Lilly Corporate Center
CITY: Indianapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 LPLYSILSALTILGMIMASAFLFF---NIKNRNQKLIKMSSPYMNNLIILGGMLSYASIF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 LFGLDGSFVSEKTFETLCTVRTWILTVGYTTAFGAMFAKTWRVHAIFKNVKMKKKIIKDQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 --LIMVGGGL-----YLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSF-LKGLLTNL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 ENTHMTIWLGIVYAY-----KGLLMLFGCF-----LAWETRNVSIPAL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.3%; Score 77; DB 3; Length 332;
21.7%; Pred. No. 0.72;
tive 31; Mismatches 69; Indels
960 PIVKSSLLYASSQALPFFCMALGFWYGGSLLGHGEYSLFQFYV 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DAPA:
APPLICATION NUMBER: US/09/183 253
                                                                                                   Sequence 4, Application US/09183253
Patent No. 6043054
GENERAL INFORMATION:
APPLICANT: STAWNER, LISA
APPLICANT: STAWNER, MCLANIE
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPENDENCE ADDRESS:
ADDRESSE: Rather & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LLGL--HLIIEK------MAWLHT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GP-70395
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APPLICATION NUMBER: 9817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 20-FEB-1998
AFTORNEY AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JMBER: US/09/183,253
30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFRAX: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Wir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.3%
Best Local Similarity 21.7%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / MOLECULE TYPE: protein US-09-183-253-4
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30
                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                        19482
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                                                                 SULT 8
-09-183-253-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRK-----EAMMGVLGITCGVMVWAGIA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ANPKALIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.3%; Score 77; DB 3; Length 859; ilarity 21.7%; Pred. No. 2.6; Conservative 31; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                COMPUTER: LEM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOGTWARE: FESTSEM COF WINGOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,253
FILING DATE: 30-CCT-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 0817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 LLGL--HLIIEK------MAWLHT------
Sequence 2, Application US/09183253
Patent No. 6043054
GENERAL INFORMATION:
APPLICANT: VAWTER, LISA
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP-70395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08612734B
; Patent No. 5914246
; GENERAL INFORMATION:
                                                                                                                                                                                   Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GF
TELECOMMUNICATION INFORMATION
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 846169
INPORMATION POR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 859 amino acids
                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                ADDRESSEE: Ratner & F
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ropology: linear; MOLECULE TYPE: protein US-09-183-253-2
                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
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US-08-612-734B-2
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| : | | : | | : | | : | | 96 IRRQEGILSGFFTIFAGLILIFEAYLWKYGLDKSVLKGTMAQVYTDLTGFRTTSFAGG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 -----LHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSG---RSFLKGL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 RKEAM-----WGVLGITCGVWV-----WAGIALLGLHLIIEKMAW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 RKEAIQRMLISLGIAILLIFAAFKLGAAGITLYNLIRLLVGSLAYLAIFGLLIYLFFFKW 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 73.5; DB 2; Length 783; 25.3%; Pred. No. 5.8;
tive 24; Mismatches 64; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Flugge, Ulf-Ingo
APPLICANT: Flugge, Ulf-Ingo
APPLICANT: Flugge, Ulf-Ingo
APPLICANT: Flugge, Ulf-Ingo
APPLICANT: Flacher, Rarsten
TITLE OF INVENTION: DNA MOLECULES WHICH CODE FOR A PLASTID
TITLE OF INVENTION: 2-OXOGLUTARATE/MALATE TRANSLOCATOR
NUMBER OF ENQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FSSLENG for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
United States of America
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/922,837
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  28,354
FR: GM10077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08750723A Patent No. 5981219
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: DICKINSON, O. TOGG
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM1C
TELECHONE: 215/994-2252
TELEFAX: 215/994-2222
                                                        ZIP: 19103-2/2-
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CAMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-922-837-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11: ||| :|
203 --RGF---AKWWEG 211
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COMPUTER READABLE FORM:
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-750-723A-2
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                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           886 FLSTETKNLSGVSGVTLGTIIMTSTTLGAAMIJALAIGWKLALVCISVVPILLACGFLRF 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     946 YMLAQFQQRSKSAYEGSASYAC------EATSAIRTVASLTREQDVWGVYHDQ 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   993 LOKOGRKSLISVLRSSLLYASSQALVFFCVALGFWYGGTLLGHHEYSIFRFFV 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 LAKSGRSFLKGLLTN---LANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76; Indels
                 APPLICANT: Skatrud, Paul L.
APPLICANT: Toblo, Matthew B.
TITLE OF INVENTION: Multiple Drug Resistance Gene of
TITLE OF INVENTION: Aspergillus Fumigatus
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 -----MMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTLIMV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chalker, Alison F.
APPLICANT: Feliu, Maria M.2.
APPLICANT: Brown, James R.
APPLICANT: Brown, James R.
TITLE OF INVENTION: NO. 5889770el Spoilie
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSE: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: ISH PC Compatible
COMBUTER: TSH PC Compatible
COMBUTER: TSH PC Compatible
COMBUTER: TSH PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,734B
FILING DATE: 08-MAR.1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Mismatches
                                                                                                                                              ADDRESSEE: Eli Lilly and Company STREET. Lilly Corporate Center, DC1501 CITY: Indianapolis STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.3%; Score 76.5; Best Local Similarity 15.9%; Pred. No. 5.3 Matches 37; Conservative 29; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Craig, Anne 1. 32,976
REGISTRATION UNBER: 32,976
REFERENCE/DOCKET NUMBER: x-9681
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-354-9570
TELEPAX: 617-354-4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-922-837-2
; Sequence 2, Application US/08922837
; Patent No. 5888770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-354-4043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  Peery, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1349 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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APPLICANT: Chalker
                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-612-734B-2
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CLASSIFICATION:
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US-09-247-373B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 ------KREAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 GAAHIGAMFTAFLSVASALGTPPFLAAIVLSFLSNLMGGLTHYGIGSAPVFYGANY---- 534
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION DATA:
APPLICATION UNBER: DE P 44 20 782.4
FILING DATE: 15-JUW-1994
ATTORNEY, AGENT INFORMATION:
NAME: James F. Haley, Jr., ESq.
REGISTRATION NUMBER: 27,794
REFERENCE/POCKET NUMBER: GFB-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08924747

Patent No. 6063570

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SOTBEAN
TITLE OF INVENTION: SOTBEAN
CORRESPONDENCE 32

CORRESPONDENCE 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DLANGARE
COUNTY: ULIMINGTON
STATE: DLANGARE
COUNTY: UNITED STATES OF AMERICA
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: TBM PC COMMATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
APPLICATION DATA:
RILING DATE:
FILING DATE:
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Best Local Similarity 20.8%; Pred. No. 4.3;
Matches 43; Conservative 24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 569 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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84 WMGY-----QMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09247373B

Sequence 8, Application US/09247373B

Patent No. 6168854

GENERAL INFORMATION:
APPLICANT: O'KEEFE, DANIEL

TITLE OF INVENTION: SOTBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FITLE OF INVENTION: SOTBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES

CURRENT FILING DATE: 1089-02-10

PRIOR APPLICATION NUMBER: US/09/247,373B

CURRENT APPLICATION NUMBER: 08/924,747

PRIOR FILING DATE: 1997-09-05

NUMBER OF SEQ ID NOS: 56

SOFFWARE: MICROSOFT Office 97

FEATURE OF SEQ ID NOS: 56

SOFFWARE: MICROSOFT Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 6.7%; Score 71; DB:
Best Local Similarity 25.0%; Pred. No. 2.2;
Matches 29; Conservative 15; Mismatches
                                                                             CL-1108
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US-09-296-715-8
; Sequence 8, Application US/09296715
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD. LINDA ARAMETHY
REGISTRATION NUMBER: 33 652
REFRENCE/DOCKET NUMBER: CL-1:
TELECOMMUNICATION INFORMATION:
TELECHONE: 302-892-8112
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          LENGTH: 234 amino acids
TYPE: amino acid
STRANDENBES: not relevant
TOPOLOGY: not relevant
WOLEGULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                              ; CLONE: SE3.03B09
US-08-924-747-8
                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRGANISM: SOYBEAN US-09-247-373B-8
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PREMENT NO. 6171839

GENERAL INFORMATION.

APPLICANT SECONGE.

PATALON WINDERFORM OF THE STANDARD COMPANY

TITLE OF INVESTIGES.

OUNTER: SECURORS:

COUNTER: DELAANE

STREET: 1007 AMERIC STATES OF AMERICA

COUNTER: DELAANE FORM:

MEDIOUN TYPE: DESERVE 3.50 INCH

WEDDIOUN TYPE: OFFERIT STATES OF AMERICA

CONSTITUTION OF THE STATES OF AMERICA

STREET: BENDAGE FORM:

MEDIOUN TYPE: OFFERIT STATES OF AMERICA

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Search completed: May 6, 2001, 14:39:24 Job time: 415 sec

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-Q-/cgn2_1/GPT0_spool/US09466935/runat_03052001_075709_14798/app_query.fasta_1.529
-Q-/cgn2_1/GPT0_spool/US09466935/runat_0305_000 -GAPEX"=4.000
-GAPEDH-0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XAROP=10.000 -XAAPEXT=0.500 -FGAPOF=0.000
-DELEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=DISSUM62 -TRANS=human40.cdi
-LIST=45 -COCALIGN=200 -THR_SCORP=PCT -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LCCAL -OUTFRT=PER -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09466935_eCGN1_L_5396 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Query length: 206
Database: GenEmbl:*
Database sequences: 1283235
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Search time (sec): 1745.950000
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gb_bal:AE004719
gb_bal:YEYPUABC
gb_bal:AE00410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jb_ba3:PACARAB
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Sequence
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sed_name: gb	gb_pat1:AX0301	177								
seq_documentation_bl Locus AX030177 DEFINITION Sequence ACCESSION AX030177 VERSION AX030177	9ck 1.	: 840 bp from Patent GI:1019039	- 4	DNA EP101	376!		PAT	16-SEP-2	000	
Σ	Escherichia Escherichia Bacteria; P	la coli. La coli Proteobacteria	teria		gamma	subdivision;		Enterobacteriac	aceae;	
REFERENCE AUTHORS TITLE	Escherichia. 1 (bases 1 to 840) Belareva, A.V., Aleshin Zakataeva, N.P. Gene and method for pr	to 840) V., Aleshin,V.P. T.P. Thod for productions	A, bc	.V., ucin	Li1	Livshits, 1-amino	,V.A., To acids	Tokhmakova, I.L	. and	
TURES	AJINOMOTO KK Loc 1.	KK (JP) Location/Qualifi 1840	ualif	iers						
CDS	0 P	/organism="Escherichia /db_xref="taxon:562" 187. :807	Esch taxon	eric :562	hia "	coli"	= +			
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BASE COUNT ORIGIN	LA 165 a	WETVVASI 192 c	FALPO	OMRRG 48 g	YOR	LAKWIDG 235 t	FAGALFAG	FGIHLIISR		
alignment_sc { percent sim	ores: Quality: Ratio:	1054.00 5.117	9 9 9	4 +		Length: Gaps:	206			
ercent at	· + - }		<u>د</u> د	<del>ا</del> د	•					
S-09-466	- 4 X X	7	:							
Align seg 1	1/1 to: AX0	AX030177	from:	٦ ۲	to:	840				
1 Met   11  187 ATG	MetLeuMetLeuPheLeuThrValAlaMetValHisTleValAlaLeuMe 	eLeuThr 	/alAla         TCGCC	Metv       ATGG	alH 	isIleva              ACATTGT	lalareum	e 17   T 236		
17 tSe     237 GAG	tSerProGlyProAspFhePhePheValSerGlnThrAlaValSerArgS 	SpPhePhe 	PheVa	1ser         CTCT	Gln  CAG	Thralav             accecre	alSerArg              TCAGTCGT	S 34   T 286		
34 er#   111 287 CCC	erarglysclualametWetGlyvalLeuGlylleThrCysGlyvalMet 	MetMetG          argargg	Lyvali          cGrcc	euG1      TGGG	YII     CAT	eThrCys          TACCTGC	Glyvalme               GGCGTAAT	it 50     336		
51 Val     337 GTT	ValtrpAlaGlytleAlaLeuteuGlyLeutisteutlefleGlutysMe 	eAlaLeul            TGCGCTG	LeuGly [[[]]]	Leuh	ist  -  ATT	eullell          TGATTAT	eGluLysM 	e 67   1 386		
67 tA)      387 GGC	tAlaTrpLeuHisThrLeuIleWetValGlyGlyGlyLeuTyrLeuCysT 	hrteulle 	emetva 	161y        GGGC	G1.y   GGT	Glyteur         GGCCTGT	YrLeuCys              ATCTCTGC	T 84   T 436		
84 rpM	rpWetGlyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSer	MetLeuA	rgG1yA	laLe	uLy 	sLysGlu	AlavalSe	ir 100		

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CDS	CDS	misc_feature gene CDS	gene	gene
137 GGATGGGTTACCAGATGCTACGTGGTGCACTGAAAAAGAGGCGGTTTCT 486  101 AlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLy 117  111	AlaserLeuPheAlaLeuProGlnMetArgArgGlyTyGlnArgLeuArgCCCGCGCGCGCGCGCGGGGTTTGCGTTGTTGTTGTTGTTG	seq_documentation_block:  LOCUS  AE005613 10592 bp DNA  BECT 25-JAN-2001  DEFINITION Escherichia coli 0157:H7 genome, contig 3 of 3, section 232 of 290.  ACCESSION AE005613 AE005174  VERSION  VERSION  BECHERICHIA coli 0157:H7.  ORGANISM Escherichia coli 0157:H7.  BACTERIA; Proteobacteria; gamma subdivision; Enterobacteriaceae;  BSCherichia.  REFERENCE I (bases 1 to 10592)  AUTHORS PORTA, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,  ROSE, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,  POSÍAI, G., Hackett, J., Kilnk, S., Boutin, A., Shao, Y., Miller, L.,  GIOCDECK, B.J., Davis, B.W.M., Lim, A., Dimelanta, B., Potamousis, K.,  ADOMAGON P. D. M. AND AND AND AND AND AND AND AND AND AND	TITLE Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 JOURNAL Nature 409 (6819), 529-533 (2001)  REFERENCE 2 (bases 1 to 10592) AUTHORS Perran N. Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Posfai, G., Hackett, G. F., Evans, P.S., Gregor, J., Kirkpatrick H.A., Posfai, G., Hackett, J., Maylew, G.F., Evans, P.S., Gregor, J., Maller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.  TITLE Direct Submission JOURNAL Submitted (22-CCT-2000) Laboratory of Genetics, University of Misconsin, 445 Henry Mall, Madison, WI 53706, USA  Location/Qualifiers Lord Conf. (2007) L	/db_xref="taxon:8334" //note="enterohemorrhagic" nisc_feature /171 //note="0-island #155; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655" gene complement(72836) /gene="25332".

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Ratio: 5.117
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="yig1"
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                                                                                                                                                                                                                                                                                                                     gene
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Strain MG1655: B3821"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 ervalPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GlyllePheAlaLeulleIleValGluThrLeuAlaTrpPheThrValVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 sGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlyS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                              1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9707 CGGTGTTCTCATTGTTGTCGGTGATAACGTTGGCACTACCGCGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 tAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysT
                                                                                                                                                                                                                                                   Length: 206
Gaps: 0
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2104. 2140
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Cocation/Qualifiers
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Direct Submission
Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, 8584

On Sep 9, 1997 this Sequence version replaced gi:1790254.
This sequence was determined by the E. coli Genome Project at the University of Misconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NGHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark Software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Allanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genesi in the E. coli Genetic Site Nos., unique In nos for the genes in the E. coli Genetic Stock Center (GGSC) database at Xale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://dgsc.biology.yale.edu). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated unformation will be available at the E. coli Genetic (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version MS4. No sequence changes. Annotation addition size periodically updated; this is version MS4. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley, added promoters, protein binding sites, and repeated seguences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of names.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 11509)
Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Yides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Blattner, F.R.
Blattner, F.R.
Blattner, G. W.
Blattner, F.R.
Direct Submissan
Submitted (16-Jakon)
Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli K12
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                               AE000458 11509 bp DNA BCT 01-DEC-2000 Escherichia coli K12 MG1655 section 348 of 400 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997)
                                                                                                                                                                                                                                                              genome.
AE000458 U00096
AE000458.1 GI:2367299
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                               9907 CATTTGATTATTTCGCGG 9924
201 HisLeuIleIleSerArg 206
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                                                                                                             seq_name: gb_bal:AE000458
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                                                                                                                                                                      (bases 1
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                                                                                           IIYEGSVESLEVGDNVGTTARWGIFALIIVETLAMFTVVASLEALFQMRRGYQRLAKW
IDGFAGALFAGFGIHLIISR"
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MHDRFCELRTAAGHPVEGGRPLVIRGAYHEILFEKDAMASVALHAIVDFFNRHNSPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4200, .4230
Chote="factor Sigma70; predicted +1 start at 4006629"
Complement(4227, .4254)
Anote="factor Sigma70; predicted +1 start at 4006612"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5494, .5523 ... Frances is start at 4007865"
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5526, .6041
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4384. ,5406
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Quality: 1027.00
Percent Similarity: 99.515
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US-09-466-935-4 x AE000458
                                                                                                                                          repeat_region
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1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17

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Escherichia coli.

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.

[ Chases I to 9114]
Daniels, D.L., Plunkett, G. III., Burland, V. and Blattner, F.R.
Daniels, D.E., Plunkett, G. III., Roule and Blattner, F.R.

From 84.5 to 86.5 minutes
Science 257 (5071), 771-778 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Date: 1 to 91414)
Plunkett, III., Burland, V., Daniels, D.L. and Blattner, F.R.
Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-1995
84.5 to 86.5 minutes.
                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                         erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 lAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuA 184
                                                                                                                                                                                     84
                                                                                                                                                                                  AlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLy
tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS
                                                            erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS ECOURRS 91414 bp DNA BCT
DEFINITION E. Coli genomic sequence of the region from
ACCESSION M87049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3572 CATTTGATTATTTCGCGG 3589
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AUTHORS
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RSPHHSASLTAMVGGGAIPGFGEISLAHNGVLFLDELPEFERRTLDALREPIESGQIH
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LEIPLPPPGILSKTVVPGESSATVKORVMAARERQFKRONKLNAMLDSPEIRQFCKLE
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/gene="f516"
/note="similar to Mg chelatase subunit of Rhodobacter
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3336. .3737
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3336. .12791
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/note="corresponds to M10313 (1.
3379. 5721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="terminator-like sequence"
complement(1585, 3135)
/gene="f516"
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/note="V00290; ECILVX(1. .2343)"
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/hote="promoter matrix score of 3336. 3676
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/function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1136.
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/gene="o137"
/codon_start=1
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1223. 1627
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/gene="o137"
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Submistated (12-FEB-1992) Donna L. Daniels, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu; Phone: 608-262-2534; Fax:
608-263-7459
On May 29, 1995 this sequence version replaced gi:148169.
This sequence was determined as part of the E. coli Genome Project
(Frederick R. Blattner, director) at the University of
Wisconsin-Madison. The entire sequence was independently determined
from E. coli MG1665. Overlaps and conflicts with other sequence
determinations are annotated. Reference [1] describes the original
sequence determination of a 91408 bp sequence. References [2], [3],
and [4] describe subsequent corrections and/or updates to that
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Organism="Escherichia coli"
// Organism="Escherichia coli"
// Strain="MG1655"
// Sub_strain="MG1655"
// Sub_strain="MG1655"
// Cone_lib="lambda library of Daniels and Blattner"
// Map="bp l at 3974 kb; 84.7 minutes"
// Note="This sequence comprises the following lambda clones: DD850(EC15-116), DD851(EC13RM4), DD854(EC15-177), DD865(EC19RM8.1), DD868(EC17RM9), DD865(EC17-221), DD866(EC17-221), DD866(EC17-280). M13Mp19 or Janus vectors were used for
                                                                                                                                                                                                                4 (bases 1 to 91414)
Rudd,K.E., Sofia,H.J., Koonin,E.V., Plunkett,G. 3rd, Lazar,S. and
Rouviere,P.E.
                                                                                                                          DNA sequence of the
                                              (bases 1 to 91414)
Blattner,F.R., Burland,V., Plunkett,G. III., Sofia,H.J. and Dantels,D.L.
Analysis of the Escherichia coli genome. IV. DNA sequence of region from 89.2 to 92.8 minutes
Nucleic Acids Res. 21 (23), 5408-5417 (1993)
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/note="corresponds to V00349 (164. .500)"
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1. .200
/mote="corresponds to K02846 (1. .200)"
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/note="predicted bend of 81 degrees"
complement(266. .862)
Nucleic Acids Res. 21 (15), 3391-3398 (1993)
93347969
                                                                                                                                                                                                                                                                                       A new family of peptidyl-prolyl isomerases
Trends Biochem. Sci. 20 (1), 12-14 (1995)
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/note="terminator-like sequence"
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/note="clone EC15-116"
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/gene="f198"
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/gene="aspT"
/note="CGSC No. 989"
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Daniels, D.L.
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/gene="trpT"
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5 (bases
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Direct Submission
Submitted (09-PEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs GLIMMER (Salzberg, S., Delcher, A., Kasif, A. and White, O. (1998) NAR 26,544-549), and GeneMark (Lukashim, A.V. and Borodovsky, M. (1998), NAR 26,107-1115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate ofhemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, Mo 63110, USA
e-mail: sclifton@watson.wustl.edu or
jspieth@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                61212 AGT. TTACTGACCAATCTCGCTAATCCGAAAGCGATTATCTACTTTGGCT 61260
                                                                                                                                                                                                                   The Salmonella typhimurium Genome Sequencing Center.
Unpublished
                                                                                                         erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp 150
                     sGlyLeuLeuThrAsnLeuAlaAsnProLysAlaileileTyrPheGlyS 134
                                                                                                                                                                                           GlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrValVa 167
                                                                                                                                                                                                                                                                                167 lAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuA 184
                                                                                                                                 /organism="Salmonella typhimurium LT2"
/strain="SGSC1412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT
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Locus syrsympi 96086 bp DNA
DBFINITION Salmonella typhimurium fragment STMD1.
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1 (bases 1 to 96086)
Washington University Genome
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Waterston, R.
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RHEQGAAMAAIGYARATGKTGVCIATSGPGATWLITGLADALLDSIPVVAITGQVSAP
FIGTDGAPQEVDVLGLSLACTKHSFLVQSLEELPRINAEAPDVACSGRPGPVLVDIPKD
FIGTAGAPQPTTVENEVAFPHAEVEQARQMLAKAQFPMLYGGGVGMQAVPALRE
FLAATKMPATCTLKGLGAVEADYPYYLGMLGMGTKRANFPVQECDLLIAVGARPDDR
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/db_xref="GI:148175"
                                                                                                                                                                                                                                                                                                   /note="CGSC No. 603; inactive in wild-type E. coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="the mutation ilv02096 joins this ORF to ilvG, restoring function missing in wild-type"
                                                                                                                                                                                         /translation="MTALLRVISLVVISVVVIIIPPCGAALGRGKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60913 GAGCCCCGGTCCCGATTCTTTTTGTCTCTCTCAGACCGCTGTCAGTCGTT 60962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
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replace(4677. .4678,"tatg")
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3458. .3556
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3458. .3556
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US-09-466-935-4 x ECOUW85
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/LIANSLATIONS.
//LIANSLATIONS.
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4934. .6580

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Complement(1506. .2354)

Complement(1506. .2354)

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(YIFA) (SP:P2798) and 95% identity with amino acids 1-80

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9801. . 11345
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Summary Statistics
Consensus quality: 230709 bases at least Q40
Consensus quality: 258916 bases at least Q30
Consensus quality: 258916 bases at least Q30
Consensus quality: 258916 bases at least Q20
Estimated insert size: 216600; agarose-fp estimation
Estimated insert size: 273689; sum-of-contigs estimation
Quality coverage: 9.54 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Unit Genome Institute.
Unratioute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
                                                                         29-JUN-2000
seq_documentation_block:
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DEFINITION Mus musculus clone RP23-359N18, WORKING DRAFT SEQUENCE, 60
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69254 a 68603 c 67231 g 68544 t 5957 others
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# 11047 12223: contig of 1177 bp in length # 12224 13492: contig of 1269 bp in length # 12224 13492: contig of 1269 bp in length # 13493 14669: contig of 1177 bp in length # 14670 15886: contig of 1177 bp in length # 15887 17089: contig of 1273 bp in length # 17090 18308: contig of 1203 bp in length # 18309 19518: contig of 1219 bp in length # 18309 19518: contig of 1219 bp in length # 19519 20710: contig of 1219 bp in length # 19519 20710: contig of 1219 bp in length # 19519 20710: contig of 1219 bp in length	of 1222 unknown of 1674 unknown of 1722 unknown of 1321 unknown of 1200 unknown	gap or unknown tength and contig of 1565 bp in a 1877; contig of 1177 bp in gap of unknown length and contig of 118 bp in gap of unknown length and contig of 1202 bp in gap of unknown length and contig of 1207 bp in gap of unknown length and contig of 1207 bp in gap of unknown length and contig of 1176 bp in gap of unknown length and contig of 1209 bp in gap of unknown length and contig of 1200 bp in gap of unknown length and contig of 1200 bp in gap of unknown length and contig of 1200 bp in gap of unknown length and contig of 1200 bp	
TCGGTGTTCTCATTGTTGTCGGTGATAACGTTGGCACTACCGCGCGCTG 30381 pGlyllePheAlaleulle.IleValGluthrLeualarrpPheThrVal 166	seq_name: gb_htg7:AC020970  seq_documentation_block: LoCUS AC020970 212936 bp DNA HTG 10-FEB-2000  DEFINITION MUS musculus clone RP23-252M21, WORKING DRAFT SEQUENCE, 144  unordered pieces. ACCESSION AC020970.1 GI:6691260  VERSTON AC020970.1 GI:6691260  VERSTON AC020970.1 GI:6691260  SETWORDS HTG; HTGS_PHASEI; HTGS_DRAFT.  SOURCE		Estimated insert size: 21236; sum-of-contige estimation Californiated insert size: 157000; pulse field gel estimation Quality coverage: 4.20x in 020 bases; pulse field gel estimation Ouality coverage: 3.10x in 020 bases; pulse field gel estimation coulity coverage: 3.10x in 020 bases; sum-of-contigs estimation + NOTE: This is a 'working draft' sequence. It currently consists of 144 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  * Disserved.* 1159: contig of 1159 bp in length as preserved.  * 1160 2363: contig of 1241 bp in length apport contig of 1241 bp in length apport contig of 1241 bp in length apport contig of 1848 bp in length apport unknown length apport unknown length apport contig of 1858 bp in length apport contig of 1858 bp in length apport contig of 1855 bp in length apport contig of 1855 bp in length apport contig of 2046 bp in length apport contig of 2046 bp in length apport contig of 2046 bp in length apport contig of 2046 bp in length apport contig of 2046 bp in length apport contig of 2046 bp in length apport contig of 2046 bp in length apport contig of 1863 bp in length apport contig of 1863 bp in length apport contig of 1863 bp in length apport contig of 1863 bp in length apport contig of 1863 bp in length apport unknown length apport unk

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868 040 163 288	64221 65421 66606 68683 70713 71896	480 620 758 908 908 190 314	5888 5888 5715 715 843 127 127 391	95449 96801 97979 99180 100438 101828 103118 104551 105855
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      seq_documentation_block:
      LOCUS
      HTG
      16-FEB-2000

      LOCUS
      AC020885
      268294 bp
      DNA
      HTG
      16-FEB-2000

      DEFINITION
      Muse musculus clone RP23-46411, LOW-PASS SEQUENCE SAMPLING.

      ACCESSION
      AC020885
      G1:6980212

      KEYWORDS
      HTG; HTGS_PHASEO.

                                                                                                                                                                  134 erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp 150
                                                                                                                                                                                                                                                                                                                              51 ValTrpAlaGlylleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMe 67
                                                                                                                                                                                                                       17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34
gap of unknown length 111662: contig of 1232 bp in length
                                                              Gaps: 0
Percent Identity: 96.602
                                                                                                                                            to: 212936
                                                  Length:
                                                                                                                                             from: 1
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                                                                                                                                           Align seg 1/1 to: AC020970
                                                 Quality: 747.00
Ratio: 3.698
nilarity: 98.058
                                                                                                      alignment_block:
US-09-466-935-4 x AC020970
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           110431
                                                                           Percent Similarity:
                                        alignment_scores:
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Month of the control	* 15873 16608: contig of 736 bp in length  * 16609 16851; contig of 243 bp in length  * 16852 17277; contig of 426 bp in length  * 17278 18057; contig of 780 bp in length  * 18058 18704; contig of 780 bp in length  * 18058 18704; contig of 780 bp in length  * 18058 18704; contig of 647 bp in length  * 18705 19414; contig of 6710 bp in length  * 18705 19414; contig of 710 bp in length  * 18705 19414; contig of 170 bp in length	20373 21010; contrig of 638 bp in length 21011 21256; contrig of 218 bp in length 22364 23639; contrig of 1016 bp in length 23640 24853; contrig of 1016 bp in length 23640 24853; contrig of 1016 bp in length 24854 25795; contrig of 1024 bp in length 24854 25795; contrig of 1024 bp in length 24856 27027; contrig of 1032 bp in length 25708 27729; contrig of 1032 bp in length 27730 28722; contrig of 1032 bp in length 27730 28722; contrig of 1032 bp in length 27731 28722; contrig of 1032 bp in length 27732 29714; contrig of 1032 bp in length 27733 28723; contrig of 1032 bp in length 27734 28723; contrig of 1032 bp in length 27735 28724; contrig of 1032 bp in length 27736 27725; contrig of 1032 bp in length 27737 28725; contrig of 1032 bp in length 27738 31398 31577; contrig of 1032 bp in length 27739 28725; contrig of 1032 bp in length 27730 28725; contrig of 1032 bp in length 27731 28725; contrig of 1032 bp in length 27730 28725; contrig of 1032 bp in length 27731 28725; contrig of 1032 bp in length 27730 3777; contrig of 1032 bp in length 27730 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 27731 3777; contrig of 1032 bp in length 2774; contrig of 1032 bp in length 2775; contrig of 1032 bp in length 2777 35903; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2777 3777; contrig of 1032 bp in length 2778; contrig of 1032 bp in le	
	house mouse.  Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 268294) DOE Joint Genome Institute. Sequencing of Mouse Unpublished 2 (bases 1 to 268294) DOE Joint Genome Institute. Direct Submission Submitted (10-JNN-2000) Production Sequencing Facility, DOE J	sequencing reacce contains 183 individual contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Lov-pass sequence sampling is useful for arbitrary. Lov-pass sequence sampling is useful for arbitrary. Lov-pass sequence sampling is useful for arbitrary. Lov-pass sequence sampling is useful for arbitrary. Lov-pass sequence sampling is useful for the contain that may be gene-rich and allows forever, it should not be sammed that this clone the record is updated, the accession number will be preserved.  1013 contig of 1013 bp in length the record is updated, the accession number will be preserved.  1014 1615 goot of or from the event that the record is updated, the accession number will be preserved.  1015 goot of or from the mapth contig of 1019 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 475 bp in length contig of 647 bp in length conti	gap of unknown leng 15872: contig of 301 bp in gap of unknown leng

us-09-466-935-4.rge

Page 14

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f unknown length
of 1403 bp in length
unknown length
of 1060 bp in length
unknown length
of 1409 bp in length
                                                                            f unknown length
g of 1445 bp in length
f unknown length
g of 1005 bp in length
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of 1592 bp in length
unknown length
of 504 bp in length
unknown length
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contig of 1005 bp in length
gap of unknown length
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of 1028 bp in length
                                       length
bp in length
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of 1042 bp in length
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gap of unknown length
contig of 499 bp in length
gap of unknown length
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unknown length
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of 243 bp in length
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unknown length
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unknown length
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Gaps: 0
Percent Identity: 98.571
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US-09-466-935-4 x AC020885/rev
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Percent Similarity: alignment\_scores:

Align seg 1/1 to reverse of: AC020885 from: 1 to: 268294

117 LysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGl 133

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. I, bases 1 to 290452)
Grills, G., Han, J., Montgomery, K.T., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Goltz, M., Goltz, J.S. and Kucherlapati, R., High Throughut Mouse Sequencing Submitted (23-AUG-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
On Aug 30, 2000 this sequence version replaced gi:9885883. 2 (bases 1 to 290452)
Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R..
Ioshkhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
Direct Submission \* NOTE: This is a 'working draft' sequence. It currently sonsists of 196 contigs. The true order of the pieces is not known and their order in this sequence record is 183 uAlaLysTrpIleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGlyI 200 rpGly11ePheAlaLeu11e11eValGluThrLeuAlaTrpPheThrVal 11343 TTCATTTGATTATTTCGCGG 11324 AC079167 AC079167.2 GI:9945047 HTG; HTGS\_PHASE1. 200 leHisLeulleIleSerArg 206 seq\_name: gb\_htg17:AC079167 AECOM house mouse. Mus musculus Web site: ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL 150 REFERENCE AUTHORS COMMENT

30.08.1 31014; contig of 834 bp in length 31015 31034, gap of inxnown length 31018 31080; gap of inxnown length 31081 31080; gap of inxnown length 31081 31080; gap of inxnown length 31081 31080; gap of inxnown length 31081	,
arbitrary. Gaps between the contigs are represented as runs of N. Dut the exact sizes of the gaps are unknown.  Balloone and 111 Persone sizes of the gaps are unknown.  Balloone and 111 Persone sizes of the gaps are unknown.  By 111 Persone and the arbitrary of the presenced.  By 111 Persone and the arbitrary of the presenced as a smilbiol and the arbitrary of	

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US-09-466-935-4 x ECORECQ
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ORIGIN
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Escherichia coli
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 2695)
Irino,N., Nakayama,K. and Nakayama,H.
The reco gene of Escherichia coli K12: Primary structure and evidence for SOS regulation
MOL. Gen. Genet. 205, 298-304 (1986)
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E.coli recQ gene complete cds, and pldA gene, 3' end.
M30198
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                            g of 873 bp in length
f unknown length
of 851 bp in length
f unknown length
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unknown length
                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 99.138
      unknown length
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/organism="Escherichia coli"
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/db_xref="taxon:562"
1. 352
/gene="pldA"
<1. 352
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61879:
62752:
62772:
63623:
63643:
64694:
                                                                                                                                                                                                                                                          559.00
4.861
99.138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AC079167
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US-09-466-935-4 x AC079167
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LOCUS ECORECO
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   61860
61880
62753
62773
63624
63644
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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KEYWORDS
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AUTHORS
TITLE
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479, .2311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 ValTrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMe 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                          486.00
4.629
98.131
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* 14027 14869: contig of 843 bp in length * 14870 15738: contig of 869 bp in length * 15739 16426: contig of 688 bp in length * 15739 16426: contig of 688 bp in length * 15739 1741: contig of 688 bp in length	17938: contig of gap of unl 18715: contig of ago of unl 18715: contig of ago of unl 18715: contig of unl 19703: co	20212: contig		gap of un 21570: contig of	gap ol unknown length  * 21571 22378: contig of 808 bp in length  * aap of unknown length	22940: contig gap of	* 22941 23943: config of 1003 bp in length * 23944 24650: config of 707 bp in length	gap of 25686: contig		* 25821 26268: contig of 448 bp in length * an of unknown length	* 26269 27152: contig of 884 bp in length * qap of unknown length	* 27153 28057; Contig of 905 bp in length * qap of unknown length	29002: contig gap of	29991: contig gap of	* 29932 30780: contig of 789 bp in length qap of uknown length * 30781 31514: contig of 734 bp in length	gap of 32152: contig	* 32153 32933; contig of 781 bp in length	* 32934 33042: contig of 109 bp in length * app of unknown length		contig gap of	35821: contig	37013:	38147: contig gap of	38852: contig gap of	* 38853 39840: contig or 988 bp in tength * 3084 AARAA, contig of 1084 br in length	gap of	43258: contig of 871 k
LOCUS AC020833 62274 bp DNA HTG 16-FEB-2000 DEFINITION MUS MUSCULUS CLONE RG-MBAC_40H2, LOW-PASS SEQUENCE SAMPLING. AC020833		REFERENCE 2 (bases 1 to 62274) AUTHORS DOE Joint Genome Institute.	JOURNAL SUBmitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA COMMENT * NOTE: This record contains 69 individual	* sequencing reads that have not been  * contigs. Runs of N are used to sepa	<pre>and the older in which they appear is completely     * arbitrary. Low-pass sequences sampling is useful for     * identifying clones that may be gene-rich and allows</pre>	* overlap relationships among clones to be deduced. * However, it should not be assumed that this clone	sequenced to completion. In is updated, the accessived.	1 296: contig of 296 bp	1049: contig or gap of un	* 1050 1812: Contrig Or /05 Dp in length  * app of unknown length  * 1813 2420: Contrix of Kns ha in length	gap of unknown le	gap of unknown 3645: contiq of 692 by	gap of unknown 1 4766: contig of 1121	unknown of 530 bg	* 5297 5584: contigo of 288 bp in length * 5297 5584: contigo of 288 bp in length *	6454: contig of gap of un	6853; contig of 399 by gap of unknown	* 6854 /566; Contig of /13 bp in length  * 7567 8253; Contig of 687 bp in length	gap of unknown 9058: contiq of 805 b	gap of unknown contig of 620	gap of unknown 10272: contig of 594 b	unknown of 618	unknown of 805 by	ot unknown ig of 982 b	* 12678 13130: contig of 453 bp in length	* 13131 13878: contig the bring headth	* 13879 14026: Sorting of 148 bp in length * app of unknown length

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complement(2427. .3239)
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May,B.J., Zhang,Q., Li,L., Paustian,M.L., Whittam,T.S. and Kapur,V.S.
Complete nucleotide sequence of an avian isolate of Pasteurella
                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. (2001) In press
2 (Dases 1 to 10184)
2 Shang, or and Kapur, V.
Direct Submission
Submitted (24-0CT-2000) Department of Veterinary Pathobiology,
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
55108, USA
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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105. 1820

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                                                                                                              multocida
                                                                                                                                                                                                                                                                                                                                                                                                                  source
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REFERENCE
AUTHORS
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JOURNAL
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Pasteurella multocida
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
1 (bases 1 to 10184)
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Pasteurella multocida PM70 section 77 of 204 of the complete
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bp in length
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                     length
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                                                                                                                                    gap of unknown is 47108: contig of 1434 by app of unknown is 48115: contig of 1007 by app of unknown is 49871: contig of 1756 by app of unknown is 1661: contig of 1750 by gap of unknown is 53728: contig of 2067 by 56784: contig of 3056 by app of unknown is 59220: contig of 3056 by app of unknown is 59220: contig of 3056 by app of unknown is 59220: contig of 3056 by app of unknown is 62274: contig of 3054 by
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16965 a 13547 c 13251 g 18170 t
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                                                                        unknown
of 1309
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contig
gap of
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gap of
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AE006110 AE004439
AE006110.1 GI:12721018
                                         44365:
                                                                                                          45674:
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US-09-466-935-4 x AC020833/rev
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LOCUS AE006110
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KEYWORDS
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Gaps: 2
Percent Identity: 37.073
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2201 c
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Percent Similarity:
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White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.

Direct Submission

Limitted (27-SEP-1997) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

The H. influenzae sequence has been updated by R. Fleischmann. New
database matches have been assigned, product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
incorporated their annotation into the /notes fields of the
corresponding H. influenzae genes

To (Tases) 12 1137)

S White,O. Clayton,R.A. Kerlavage,A.R., Fleischmann,R.D.,
Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.

Direct Submission

N. Submitted (28-MAY-1998) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

The whole genome was shifted by 588 nucleotides for a new start

On Oct 1, 1996 this sequence version replaced gi:1222062.

Location/Qualifiers

Ince
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Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,

Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,

Fleischmann,R.D., Adams,M.D., Fleisch, Tomb,J., Dougherty,B.A.,

Merrick,J.M., McKenney,K., Sutton,G.G., FitzHugh,W., Fields,C.A.,

Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E.,

Cotton,M.D., Utterback,T., Hanna,M.C., Nguyen,D.T., Saudek,D.M.,

Brandon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L.,

Geoghagen, N.S., Gnebm,C.T., McDonald,L.A., Small,K.V., Fraser,C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S.,
Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S.,
Borodovsky,M., Rudd,K.E. and Koonin,E.V.
Metabolism and evolution of Haemophilus influenzae deduced from a
Whole-genome comparison with Escherichia coli
Curr. Biol. 6 (3), 279-291 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-JUL-1995) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases I to 11137)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U32810 11137 bp DNA BCT 29-MAY-1998
Haemophilus influenzae Rd section 125 of 163 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Raemophilus.
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White, O., Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                   3495
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                                                                                                  3688 ACCTTATGTTAAAAAGT.....CAACAAAATGTGGTTTTCGAGCCAGTT 3645
                                                                                                                                                                                                                 3644 TCTGAACAAGAACAAATAAACAGACCAGCATCAAAAAAGAAATCACCAA 3595
                                         87 yrGlnMetLeuArgGlyAlaLeuLySLySGluAlaValSerAlaProAla 103
                                                                                                                                                                                                                                                                                                                                                                                      134 erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrValVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 lalaSerLeuPhealaLeuProGlnMetargArgGlyTyrGlnArgLeuA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 laLysTrpIleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGlyIle 200
                                                                                                                                                                                                                                                                                                                                                                                                                     104 ProGlnValGluLeuAlaLysSer.....GlyArgSerPheLeuLy
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Science 269 (5223), 496-512 (1995)
95350630
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Haemophilus influenzae Rd
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U32810 L42023
U32810.1 GI:1574760
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LOCUS U32810
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96398784
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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                                 percent
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putative"
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identity: 54.41; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4194 AGGGCCTGATTTCTTTTATGTAAGTCGAATGGCGGCAAGTAACTCTCGTC 4243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ## 111111::111111 | FIRE | 111::: | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1294 GGAATGCTTTCTATGTTGGGATTGGCGGTGTTGTTCGTTACCATTCCAGC 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 TrpGlyIle......PheAlaLeuIleIleValGluThrLeuAlaTr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 lyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaPro 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AlaProGlnValGluLeuAlaLysSer......GlyArgSerPheLe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 uLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 pPheThrValValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 yrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGlyAlaLeuPheAla 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
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                                                                                                                                                                                                                       /product="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4244 GTAATACAGTTTGTGGCATTTTAGGCATAGCCTTGGCATCGCCTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368.50 Length: 207
2.457 Gaps: 4
72.464 Percent Identity: 38.647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 11137
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5876. .6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: U32810 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-466-935-4 x U32810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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4796. 15608
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LIGIAHYAIDLSPGILISDLGHILERSGCSARENELTALPLESSIINKYDRYDARDFALE
GGEDYELCFTIPPEXKDELELRIKKLNVPCTCIGKINNFGOBFSPFFLEDGRFVNITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="phosphatidylglycerophosphatase A (pgpA)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:D10483 SP:P04036 GB:M10611 PID:145710 PID:216458 percent identity: 69.74; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWFADIGERVEISHKASSRAFFANGAVRAGKWLENKANGLFDATDVLDLNNL.
Complement(5503. .5851)
Gene="H11309"
complement(5603. .5851)
/gene="H11309"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGURE 11786620 PID:1773102 PID:1786620 PID:2329841 percent identity: 47.77; identified by /codon_start=1 /trans_table=11 /trans_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4147. 4779
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4147. 4779
//gene="H11307"
//note="similar to GB:U00096 SP:P75693 PID:1657525
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PID:1786619 PID:2329840 percent identity: 53.09;
identified by sequence similarity; putative"
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AATGVATHREGY IKVDEEDTNINVASITVGVGDIMBGGIELFPYAVKARGNGLSERLENNK
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PCKNKLVCAGPEETVVGLHGIGFAVDEMIQGFGVAMKMGATKADFDSVVAIHPTGSEE
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1 (bases 1 to 11321)
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                                                                                                                                                                                                                                                                                                               seq_documentation_block:
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DEFINITION Vibrio cholerae chromosome I, section 17 of 251 of the complete
Submitted (14-JUN-2000) The Institute for Gamedical Center Dr. Rockville, MD 20850, USA Location/Qualifiers

    11321
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AE004109.1 GI:9654590
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//iotce=/identified by Glimmer2; putative\*
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1 (sites)
Takami, H., Nakasone, K., Hirama, C., Takaki, Y., Masui, N., Fuji, F.,
Takamura, Y. and Inoue, A.
An improved physical and genetic map of the genome of alkaliphilic
Bacillus sp. C-125
Extremophiles 3 (1), 21-28 (1999)
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Takam,H., Nakasone,K., Ogasawara,N., Hirama,C., Nakamura,Y.,
Masui,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K.
Sequencing of three lambda clones from the genome of alkaliphilic
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Bacillus/Staphylococcus group; Bacillus.
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DEFINITION Bacillus halodurans genomic DNA, section 11/14.
ACCESSION AP001517 BA000004
          to: 11321
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       to reverse of: AE004109 from: 1
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LVGLSLTWFSCLAWLLTTSAMQORMQRITRSVDSICAAVFILAGSVILMONSRALAOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVYWDAKKKALTTFDGRETAPLNATPELFLDSTGQPMKFYDAVVGGRSVOTPGTVKLL.
WETHRQYGKLEWARLIEPVAKLAEQGFEVSPRLAALIAEDKERLGRFPATKAYFFDAQ
GEPLTAGTLLKNPDYAATLRAIAQQGASAFYQGDIAKDIIATVQNAPGNPGVLAQOF
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LGDASQLAFADRGLYMADQDYPVPTQGLLDKTYLAERAKLIQPGKALTSAPAGNPPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:AL123456; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GP:3294250; identified by sequence similarity; putative" /codon start=1 /transl_table=11
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Percent Identity: 31.313
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/gene="VC0194"
                                                                                                                                                                                                                                                                                                                                /gene="VC0192"
complement(8485. .9297)
/gene="VC0192"
complement(7742. .8410)
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/codon_start=1
/transl_table=11
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/transl_table=11
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/transl_table=11
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US-09-466-935-4 x AE004109/rev
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GCMPLGment(3074, 4309)
                                                                                                                                                    AKPSNNFVLSYERYKOYLKELKOVFKSFYFHEKELYHTLQAIGTNKEELISQTCTLIC
KYNETLKSIRKLDQLFQTSYMDDIQALHIQHQKELEALGLLLNDNGTLTLNSDVFRCQ
LSTSDQDTMAVLKRFKSLLLKQYHTISQLQVPNSHQMSPYDPPGEPLKGFIIEEKG"
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FPMKVAEPWEFPPTHIDKEBARKMDRFTQFAASALMEKDADLETFBIARRVGV
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TACASGANSIGDARKVIORGDADVMITGGABAPITNMAVAGFSMAKAISTSEDPNTAS
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GAARAMKQAIEDAGLTPEDIQYMNAHGTSTYYNDKYETLAAKQVFGDHVNNLAISSTK
SMTGHLLGAAGAVEAIFSVKAIEEGIIPPTINYETPDPDCDLDYVPNEARKQGVNAVL
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/transl_table=11
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/gene="BH2883"
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1694. .2977
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Extremophiles 4 (4), 209-214 (2000)
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Takami, H. and Horikoshi, K.
Reidentification of facultatively alkaliphilic Bacillus sp. C-125
to Bacillus halodurans
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Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Sasaki, R., Masui, N.,
Fuji, F., Hirama, C., Nakamura, Y., Ogasawara, N., Kuhara, S. and
Horikoshi, K.
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Takami, H. and Horikoshi, K.
Analysis of the genome of an alkaliphilic Bacillus strain from industrial point of view
Extremophiles 4 (2), 99-108 (2000)
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Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999) 99356711
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Takani, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G.,
Sasaki, R., Hirama, C., Fuji, F. and Masui, N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans C-125
                                                                                                                                  , Takaki, Y., Nakasone, K., Hirama, C., Inoue, A. and
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Bacillus sp. strain C-125
Extremophiles 3 (1), 29-34 (1999)
99184646
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249-284; Springer-Verlag (1999)
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Takami, H. and Takaki, Y.
Direct Submission
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/gene="BH2879"
                                                                                                3 (sites)
Takami,H., T
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Takami,H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52263 TITITIACGATICAACIAITAGGAGCIGCITAITTAATITGGITAGGIT 52312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52363 GAAACACAACCAATCCAACAAAAGATAGTAAATCATCCATACAAGG 52412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 ProAlaProGlnValGluLeuAlaLysSerGlyArgSer...... 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YrGlnMetLeuArgGlyAla.....LeuLysLysGluAlaValSerAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 yProAspPhePhePheValSerGlnThrAlaValSerArgSerArgLysG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 GlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMetAlaTrpLe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52213 ACATATACAGTACTGGATTTGCTTTTTAATTGAAACATATCCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 luAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292.00 Length: 207
2.147 Gaps: 2
65.700 Percent Identity: 32.367
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                                                                                                           unknown"
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US-09-466-935-4 x AP001517
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Mon May 7 11:08:15 2001

1.96 13.85 20.69 2.91 2.91

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Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aleshin VV, Belareva AV, Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-threonine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-threonine, which accumulates. The accumulated amino acids can then be removed from the culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterium of the present invention may also be used to synthesise pmoserine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli. This sequence may be used to impart L-threonine resistance on E. coli bacteria, which would be useful for producing a high yield of L-threonine. L-threonine resistance means that the bacteria will be able to grow on a minimal medium containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the L-threonine resistance gene, rhtC, from
      150.33
135.07
131.94
147.25
        81.00
81.00
80.50
80.00
80.00
                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A48443
                                                                                                                                                                                                                                                                                L-threonine synthesis; rhtC;
L-leucine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 840 BP; 165 A; 192 C; 248 G; 235 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 206
Gaps: 0
Percent Identity: 100.000
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/SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:Z12313
                                                                                                                                                                                                                                               coli L-threonine resistance gene, rhtC.
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
187..807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Page 14-15; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              /product= "RhtC"
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                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99EP-0125406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98RU-0123511
                                                                                                                                seq_documentation_block:
ID A48443 standard; DNA; 840
                                                                                                                                                                                                                 08-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                L-threonine resistance;
                                                                                                                                                                                                                                                                                               L-homoserine; L-valine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 5.117
Percent Similarity: 100.000
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US-09-466-935-4 x A48443
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P-PSDB; Y99598.
                                                                                                                                                                                                                                                                                                                               Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1013765-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1998;
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                                                                                                                                                    1668
1068
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2114
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2.3e-22
8.4e-14
5.8e-12
5.8e-12
3.0e-05
3.1e-05
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10.19
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202.58
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137.46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Database sequences: 678276
Database length: 291890651
Search time (sec): 172.640000
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Query: US-09-466-935-4
                                                                                                            Command line parameters:
                                 3:43
                               Date: May 6, 2001
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l production; excretion protein gene;
ds.
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                                                                                                                                                                                                                                                                                                                                                                 lAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuA 184
                                                                                                        29
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                                                                                                                                                                                                                                                                                                                                       187 ATGTTGATGTTATTTCTCACCGTCGCCATGGTGCACATTGTGGCGCTTAT
                                                                                                                                                      387 GGCCTGGCTGCATACGTGGCTGGCGGTGGCCTGTATCTCTGCT
                                                                                                                                                                                                                  sGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlyS
                                                                                                                                                                                                                                                                 erValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrP
                                                                                                                                                                                                                                                                                                                             GlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrValVa
MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe
                                  17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS
                                                                                                                                             tAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysT
                                                     237 GAGCCCCGGTCCCGATTTCTTTTTTTTCTCTCAGACCGCTGTCAGTCGTT
                                                                                                         51 ValTrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..672
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/product= "Yahn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. coli; yahN gene; amino acid
amino acid excretion protein; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                        HisLeuIleIleSerArg 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID A52688 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
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The present sequence is the yahN gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in lysine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                       production of L-amino acids by an Escherichia bacterium increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                       Ψ,
                                                                                                                                                                                                                                                                       Nakanishi K, Aleshin VV, Troshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 CAGGGGTGCTGACCGGGCTGGGCGTGGGCGTGCGTTTTATTCC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 yrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaProAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 CCGCAAATGAGCACACTACAACAACCGATTAGCGCCCCCTGGTATGTCTT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 .PheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 yProAspPhePheValSerGlnThrAlaValSerArgLysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 lualametMetGlyValLeuGlyIleThrCysGlyValMetValTrpAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 GGGTTGGTTTGTTTGGTCTTGCAACGCTAATTACGCAGTGTGAGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 uHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 206
Gaps: 3
Percent Identity: 28.155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 672 BP; 130 A; 154 C; 178 G; 210 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlnValGluLeuAlaLysSerGlyArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 17-18; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to:
                                                                                                                                               98RU-0124016.
99RU-0104431.
                                                                                              99EP-0125263
                                                                                                                                                                                                                                                                       Zakataeva NP,
                                                                                                                                                                                                                           (AJIN ) AJINOMOTO CO INC
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1.937
65.534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-466-935-4 x A52688
                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-414802/36
P-PSDB; B01786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 GGTGCAGCATGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                    Tokhmakova IL;
EP1016710-A2
                                                                                                17-DEC-1999;
                                                                                                                                                  30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                          Livshits VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                 05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                            Increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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the gene are transfected into a bacterium. The bacterium used is E.
                                Sequence 639 BP; 142 A; 128 C; 161 G; 208 T; 0 other;
                                                                                                                                                                                                          to: 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID A61501 standard; DNA; 1668 BP.
                                                                                            Quality: 190.00
Ratio: 1.624
Percent Similarity: 57.921
                                                                                                                                                                                                          Align seg 1/1 to: A52689
                                                                                                                                                           alignment_block:
US-09-466-935-4 x A52689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 CGACTG 621
                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A61501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the yeas gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increase decumulation of amino acids in the cell. In this case, an increase in lysine, alamine, valine, histidine, isolaucine, glutamic acid and proline is achieved if multiple copies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coli; yeas gene; amino acid production; excretion protein gene;
181
                                                                                                                                                                                                                                                                       581 GGCGTATGCAACGCGTTGCCAGTCGGGTTATTGGTGCAATTATTGGTGTA 630
                                                 131 yrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThrThr 147
                                                                                                                                                                                                                                       181 InArgLeuAlaLysTrpIleAspGlyPheAlaGlyAlaLeuPheAlaGly 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakanishi K, Aleshin VV,
                                                                                                                                AlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAlaTrpPh
                                                                                                                                                                           eThrValValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrG
                                                                                                                                                                                                      531 AGTITITCTTAGTCAGGCGTTTTCTTTGCCCGCTGTGCGTCGTGCTTATG
                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid excretion protein; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Yeas"
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99RU-0104431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli yeas gene.
                                                                                                                                                                                                                                                                                                                       631 TTCGCGCTACGCCTGATT 648
                                                                                                                                                                                                                                                                                                      198 PheGlyIleHisLeuIle 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID A52689 standard; DNA; 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
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09-MAR-1999;
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protein -
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427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 rgGlyAlaLeuLysLysGluAlaValSerAlaProAlaProGlnValGlu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 aAsnProLysAlaIleIleTyrPheGlySerValPheSerLeuPheValG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 lyaspasnValGlyThrThralaArgTrpGlyIlePheAlaLeuIleIle 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 ValGluThrLeuAlaTrp......pheThrValVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 lalaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuA 184
                                                                                                                                                                                                                                                                                                                                                                102 ragegreagragegrargaaagecggrarcraecgecreecgrerar 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                52 ATTTTTATTGTGTTGGTGCCAGGGCCAAATACCCTGTTTGTACTCAAAAA 101
                                                                                                                                                                                                                    13 IleValAlaLeuMetSerProGlyProAspPhePhePheValSerGlnTh 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 ACGCGACCCTGAAGGTAAAATAGCGAGCCCAAATCCGATGAGCCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 rAlaValSerArgSerArgLysGluAlaMetMetGlyValLeuGlyIleT
                                                                                                                                                                                                                                                                                                                                                                                                                      46 hrCysGly......valMetValTrpAlaGlyIleAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 LeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLeuHisThrLeuIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 TTA.....ATTAAGACCACCCGATATTATTCAACATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 eMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 LeuAlaLysSerGlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAl
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                     Gaps: 6
Percent Identity: 28.218
Length:
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    A. vitis hypersensitive response elicitor-encoding DNA, SEQ ID NO:6.

                              Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant; ds.
                                                                                                                                                      WPI; 2000-376567/32.
P-PSDB; B11630, B11631, B11632, B11633, B11634.
                                                                                                                                         Zhang H;
                                                                                                                           (CORR ) CORNELL RES FOUND INC
                                                                                                  99WO-US26079.
                                                                                                               98US-0107387.
     (first entry)
                                                                                                                                         Burr IJ, Herlache IC,
                                                          Agrobacterium vitis
                                                                       WO200028056-A2
     23-OCT-2000
                                                                                                               06-NOV-1998;
                                                                                                 05-NOV-1999;
                                                                                    18-MAY-2000
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Sequences A61501-A61524 represent nucleotide sequences encoding
Agrobacterium vitis hypersensitivity response (HR) elicitor proteins
(B1630-B1688). The HR is a rapid, localised necrosis that is
(B1630-B1688). The HR is a rapid, localised necrosis that is
cubically second to be a rapid and element of the pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in alling-off and killing of the pathogen. On grape plants, the A. vitis HR elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistence. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistence to disease, such as those caused by fundy, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to cold, and to impart resistence to environmental stresses, e.g., cold, and to impart nesistence to environmental stresses, e.g., cold, and to impart nesistence to environmental stresses, e.g., cold, and to impart per encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and encodes and encodes and encodes and encodes and encodes and encodes and encodes and encodes and elicitor proteins, may allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents or polluting New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of a hypersensitive response Claim 7; Page 82; 157pp; English.

Sequence 1668 BP; 441 A; 423 C; 462 G; 342 T; 0 other;

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6 LeuThrValAlaMetValHisIleValAlaLeuMetSerProGlyProAs
          Length: 200
Gaps: 5
Percent Identity: 27.000
                                                                                                            from: 1
                                                                                                            to reverse of: A61501
                                                                  alignment_block:
US-09-466-935-4 x A61501/rev
                        1.471
61.000
            179.50
                                     Percent Similarity:
                           Ratio:
alignment_scores
                                                                                                           Align seg 1/1
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22

Burr IJ, Herlache TC, Zhang H; (CORR ) CORNELL RES FOUND INC

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A. vitis hypersensitive response elicitor-encoding DNA, SEQ ID NO:11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
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                                                                                                                                                                                                                                                                        etLeuArgGlyAlaLeuLysLys........GluAlaValSerAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                   yLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlyServ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 CGTTTCGACCTTTTTGTCCAACCCGGCCATTCGAACCGTCGTGCTGCGTC 180
                                                                                     :: :::||||||||::: :::|
502 TGGCGCCTCGAFGGGCATTGCCTATCTAT
                                                                                                                                                                                                                                                                                                                                                                     111 CCCAGCGACAGA.......TCGATGGGCCGGGAATGATGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                            323 TCTACACGCAATTCATCGGCAAGGACACGCCGCTGTCTCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 GCCAGCGCCTGTTCAATATCCTGATCGGGGTCGTGCTCGCCTCGCTGGGGG
pPhePheValSerGlnThrAlaValSerArgSerArgLysGluAlaM
                               652 TITIGCCAIGGIGICGCGCAAIAGIITICIIIIAIGGCCGCAAAICCGGGC
                                                                   etMetGlyValLeuGlyIleThrCysGlyValMetValTrpAlaGlyIle
                                                                                                                                      AlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLeuHisTh
                                                                                                                                                            72 rLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnM
                                                                                                                                                                                                                                                                                                                                                ProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 lValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgL
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                                                                                                                                                                                                                                          502 TATCATCAAATTCGTCGGCGCGCCTATCTGGTCTATGCGGGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200028056-A2
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Sequences A61501-A61524 represent nucleotide sequences encoding
Agrobacterium vitis hypersensitivity response (HR) elicitor proteins
(B1630-B1688). The HR is a rapid, localised necrosis that is
(B1630-B1688). The HR is a rapid, localised necrosis that is
consisted with the active defence of plants against many pathogens, and
cocurs when a pathogenic organism interacts with a nonhost plant (i.e.
one in which intracellular bacterial growth and disease development do
not occur). Like other HR elicitors, the A. vitis elicitor functions in
non-host plants by causing a rapid hypersensitive response that results
on non-host plants by causing a rapid hypersensitive response that results
in non-like other HR elicitors, the A. vitis elicitor function of pathogen resistance. A. vitis HR elicitor
of plant cells and induction of pathogen resistance. A. vitis HR elicitor
proteins, in non-infectious form, are used to treat plants or their seeds
to impart resistance to disease, such as those caused by fungi, bacteria
or viruses; and to enhance growth, e.g., to increase yield or to provide
control insects, to impart resistance to environmental stresses, e.g.,
cold, and to improve nutritional value, e.g., altered oil content. The
same effects can be produced by producing transgenic plants or seeds by
control insects can be produced by producing transgenic plants or seeds
incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of
control of previously untreatable diseases; provide systemic treatment;
control of previously untreatable diseases; provide systemic treatment;
                                                                                                       of
                                                                          New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eliminate the need for biological control agents or polluting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1017 TITTGCCATGGTGTCGCGCAATAGTTTTCTTTATGGCCGCAAATCCGGGC 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1167 TATCATCAAATTCGTCGGCGCGCCTATCTGGTCTATGCGGGC...... 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1210 ..Trggccacggccrrcagcaagaracgcgargrcgaaggcagrcrggrr 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 etLeuArgGlyAlaLeuLysLys.......GluAlaValSerAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 ProAlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LeuThrValAlaMetValHisIleValAlaLeuMetSerProGlyProAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 pPhePhePheValSerGlnThrAlaValSerArgSerArgLysGluAlaM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 etMetGlyValLeuGlyIleThrCysGlyValMetValTrpAlaGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 rLeulleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 AlaLeuLeuGlyLeuHisLeuIleIleGluLySMetAlaTrpLeuHisTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1668 BP; 342 A; 462 C; 423 G; 441 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 200
Gaps: 5
Percent Identity: 27.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 1668
WPI; 2000-376567/32.
P-PSDB; B11635, B11636, B11637, B11638.
                                                                                                                                                                               Claim 7; Page 86~87; 157pp; English.
                                                                                                                               hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 179.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: A61502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block;
US-09-466-935-4 x A61502
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Novel RhtB protein, useful for generation of L-homoserine resistance in Escherichia bacteria and large-scale production of e.g. L-homoserine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a //*tag= a //note= "a DNA sequence corresponding to the coding region (minus the stop codon) is specifically claimed in Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1296 TATTCTGACCAATGGTCTCAATCCGAAGACGTCGATTTTCGTGATCAGTC 1345
                                                                                                                                                                         1396 TGGGGCCTGTTC.....ATCTCCCTGTCGCATTTGCTGTGGTTCGCATC 1439
yLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerV 135
                                                                                                                                                                                                                                                                                                                                                                                          166 lValAlaSerLeuPheAlaLeuProGlnMetArgArgGlyTyrGlnArgL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homoserine resistance; rhtB gene; L-homoserine; L-alanine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1440 CGTTTCGACCTTTTTGTCCAACCCGGCCATTCGAACCGTCGTGCTGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 eualaLysTrpIleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGly
                                                                                                                                   135 alPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArg.....
                                                                                                                                                                                                                                                                TrpGly11ePheAlaLeuIleIleValGluThrLeuAlaTrpPheThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT: 294405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli rhtB gene imparting homoserine resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-isoleucine; L-valine; L-threonine; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
557..1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 10-11; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294405 standard; DNA; 1200
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P-PSDB; Y79298.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-1999;
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copy number or increasing the expression rate of the rhtB DNA, the DNA being carried on a multicopy vector or on a transposon; and a method for producing an amino acid by cultivating the bacterium in a culture medium to produce and accumulate the amino acid in the medium, from which it is recovered. The method is used for the production of L-homoserine, L-alanine, L-isoleucine, L-valine or L-threonine (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 gSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 leTyrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThr 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSerGlyAr 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 ThralaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAlaTr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772 AGTGTTGAAGTGG.......GCAGGCGCGCGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 euGlyIleThrCysGlyVal.....Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         722 GGTTGGCGTGGGGTTGGGACGCTATTTCCCGCTCAGTGATTGCGTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 euCysTrpMetGlyTyrGlnMetLeuArg.....GlyAlaLeuLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 pPheThrValValAlaSerLeuPheAlaLeuProGlnMetArgArgClyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1059 CTCAACGGATTGCTCTATGGATTAAAGGACCAAAGCAGATGAAGGCGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 MetValHisIleValAlaLeuMetSerProGlyProAspPhePheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1SerGlnThrAlaValSerArgSerArgLysGluAlaMetMetGlyValL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATCGCTGGCCTCTACTCAATCGCGTCGACATTTG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                674 ..GGCGTCTATTGCTGGGCTTCAGACCGGACTGGCGATTCATATTGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 ValTrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIle......Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 yrGlnArgLeuAlaLysTrpIleAspGly......
                                                                                                                                                                                                                   Sequence 1200 BP; 285 A; 309 C; 305 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                       Length: 219
Gaps: 8
Percent Identity: 21.005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                637 TATGACCACCTCGCTCAACCACGGTTATCCGGCCGGT
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                                                                                                                                                                                                                                                                                                       122.00
1.119
49.772
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US-09-466-935-4 x Z94405
                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
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The present sequence is the L-homoserine resistance gene, rhtB, from Escherichia coli. This sequence may be used to impart L-homoserine resistance on E. coll bacteria, which would be useful for producing a high yield of L-homoserine. L-homoserine resistance means that the bacteria will be able to grow on a minimal medium containing L-homoserine at a concentration at which the corresponding wild-type strain would not grow. Since the transformed bacteria can grow on the minimal medium, it can synthesise L-homoserine, which accumulates. The accumulated amino acids can then be removed from the culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Escherichia bacterium having enhanced L-threonine resistance due to enhanced RhtC protein activity, used to produce L-threonine, L-homoserine, L-valine and L-leucine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tokhmakova IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The bacterium of the present invention may also be used to synthesise L-threonine, L-valine and L-leucine at increased levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belareva AV,
                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A48442
                                                                                                                                                                                                                                L-homoserine resistance; L-homoserine synthesis; rhtB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1231 BP; 291 A; 319 C; 311 G; 310 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 219
Gaps: 8
Percent Identity: 21.005
                                                                                                                                                                                                  E. coli L-homoserine resistance gene, rhtB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1231
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
557..1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 12-13; 24pp; English.
                                                                                                                                                                                                                                                 L-threonine; L-valine; L-leucine;
                                                                                                                                                                                                                                                                                                                                                         "RhtB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: A48442 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98RU-0123511.
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/product= "
                                                                                                                                                                      (first entry)
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                                                                                                          A48442 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AJIN ) AJINOMOTO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-414602/36.
                                                                                           seq_documentation_block
                                                                                                                                                                                                                                                                               Escherichia coli.
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                            1159 GGCGAGG 1165
204 eSerArg 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Livshits VA,
                                                                                                                                                                      08-SEP-2000
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10 MetValHisIleValAlaLeuMetSerProGlyProAspPhePheVa 26

us-09-466-935-4.rng

CHANNEL OF THE PROPERTY OF THE	PT FT	XX PN PN PD	X & X & E	P Y X X X X X X X X X X X X X X X X X X	XIX	* X E E !	rxx xxx S9 xxx		00 % 8 8		q fa	D 4								
587 637 637 637 637 637 637 637 63	m	MetMetGlyValL 43			euHisThrLeuIleMetValGlyGlyGlyLeuTyrL :::   :::    GCAGGCGGGGTTACT	96	laLysSerGlyAr	gSerPheLeulysGlyLeuLeuThrAsnLeuAlaAsnProLysAlallel     :::::::::		leValGluThrLeuAlaTr 163			204	206 116	9	720	106767;	Mel-linked mlgA gene.	electable marker; oyster larva settlement; melanin; p-hydroxyphenylpyruvate-hydroxylas	

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Novel gene encoding marine mela from Shewanella - useful as selectable marker in genetic engineering and for inducing larval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The 5' end of an open reading frame (T06767) was identified directly downstream of the Shewanella colwelliana melA gene (T06766), and was designated m19A (mel-linked gene). The role of the encoded protein (R87527) was unclear as deletion subcloning in E. coli demonstrated that only melA was required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 GTCGCCAGTATGATGATGTATCCACAACTCTTCGATATTTTAAAATG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 CATGACTCTCGGTATGACTATCGGTGTGCGCCCGAACCTTATGGATGATGG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 laLeuLysLysGluAlaValSerAlaProAlaProGlnValGluLeuAla 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 AAGGGAAAATGGCCAACCTTGACAATACCTCCAGTCAGATC.....418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 euGlyIleThrCysGlyValMetValTrpAlaGlyIleAlaLeuLeuGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 LeuHisLeuIleIleGluLysMetAlaTrpLeuHisThrLeuIleMetVa 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 .......AlaValSerArgSerArgLysGluAlaMetMetGlyValL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 720 BP; 180 A; 165 C; 165 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ProAspPhePheValSerGlnThr.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 7
Percent Identity: 25.123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Fig 14; 47pp; English.
                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                       93US-0148945.
90US-0496804.
92US-0974837.
                                                                                                                                                             900S-0496804
154..159
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .lignment_scores:
Quality: 111.50
Ratio: 0.987
Percent Similarity: 55.665
                                                                                                                                                                                                                                                                                                                                            Fuqua WC, Weiner RM;
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US-09-466-935-4 x T06767
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-039515/04.
P-PSDB; R87527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for melanogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oyster settlement
                                                                                                                                                                                                     08-NOV-1993;
21-MAR-1990;
10-NOV-1992;
                                                                                                                                                             21-MAR-1990;
                                                                     US5474933-A
                                                                                                                 12-DEC-1995
    RBS
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Page

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The MelA protein can be used as a UV blocker in sunscreen, pigment and dye compositions useful in cosmetic applications, as tints for glass or in paints and coatings for plastics, synthetic resins and fabrics, rubber and wood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 laLeuLysLysGluAlaValSerAlaProAlaProGlnValGluLeuAla 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nProLysAlaIleIleTyrPheGlySerValPheSerLeuPheValGlyA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 CATGACTCTCGGTATGAGTATCGGTGTGCGCCGAACCTTATGGATGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 GluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeuProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysTrplleAspGlyPheAlaGlyAlaLeuPheAlaGlyPheGlyIleHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 CCGACCITITITICGICICAATIACACCAGGIAIGIGIAIGACACIGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 euGlylleThrCysGlyValMetValTrpAlaGlylleAlaLeuLeuGly :::!!! ::::!!! ::::!!!!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuHisLeuIleIleGluLysMetAlaTrpLeuHisThrLeuIleMetVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGACCAAGCGATTGCACCACAATTAATGGTATTACTGTCAATTATTATG
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                                                                                                                                                                                                                                                                            Sequence 720 BP; 180 A; 165 C; 165 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 203
Gaps: 7
Percent Identity: 25.123
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US-09-466-935-4 x V08533
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                                               8 X C C C C C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes the Shewanella colwelliana MigA protein, which is related to the MelA protien of the invention. The invention relates to MelA proteins from marine bacterium of the genus Shewanella, Vibrio or Hyphomonas. The MelA protein is active in catalysing production of melanin synthesis, as well as components of marine exopolysaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marine bacterium; melanin synthesis; marine exopolysaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MelA melanin protein from marine bacteria - useful as UV blocker e.g. cosmetics % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) +\frac{1}{2}\left( \frac{1}{2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
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                                                                                         125 nProLysAlaIleIleTyrPheGlySerValPheSerLeuPheValGlyA 142
                                                                                                                                                                                        466 TCCAAAAGGCTGGGCCTTTATGATCTCGCTGCTCCCCCCTTTTATCAGCG
                                                                                                                                                                                                                                                                                                                                                                                516 TIGACCAAGCGATIGCACCACAATTAAIGGTATTACTGTCAATTATTAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 GluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeuProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 nMetArgArgGlyTyrGlnArgLeu.....AlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601 ....CGGCGGAAACCCTTAAACTGTTTTAAGTCGAGGCGATAACATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 spAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLeuIleIleVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. colwelliana MlgA coding sequence.
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90US-0496804.
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93US-0148945.
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ID V08533 standard; DNA; 720
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21-MAR-1990;
10-NOV-1992;
08-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5846531-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fugua WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V08533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MlgA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202
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327

93

92

227

177

29

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:T96816
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565 175

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1433 CGGGTTTGGGTAAAGCCCATGTTGATGGCAATCGTGCTGACCTGGTTGAA 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   072 GTCCATCGGACCGCAGAATGTACTGGTGATTAAACAAGGAATTAAGCGC. 1120
                                                                                                                                                                                                                          .....GAAGGACTCATTGCGGTTCTTCTCGTGTGTTTAATTTCTGAC 1162
                                                                                                                                                                                                                                                                                                                            1163 GTCTTTTTGTTCATCGCCGGCACCTTGGGCGTTGATCTTTTGTCCAATGC 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1292 GCCATGACAAACAAG......GTGGAAGCGCCACAGATCATTGAAGA 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1333 AACAGAACCAACCGTGCCCGATGACACGCCTTTGGGCGGTTCGGCGGTGG 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..... Gregeegegearacegegacaccegacegregarriregeeger 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 reseccedadearrereacececcecretecasececaagereresec 1660
  .....PheLeuLysGlyLeuLeuThrAsnLeuAlaAs 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 LeuileileValGluThrLeuAlaTrpPheThrValValAlaSerLeuPh 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......AlaL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 euPheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePheAla 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euProGlnMetArgArgGlyTyr.....GlnArgLeuAlaLysTrplle 187
                                                                                                                                                                                                                                                                                                                                                                              ......IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetV 76
                                                                        tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 alGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGly 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nProLys......AlaIleIleTyrPheGlySerValPheSerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 AlaLeuLysLysGluAlaValSerAlaProAlaProGlnVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 laLysSerGlyArgSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||:::
|1483 CCCGAATGCGTATTTGGACGCGTTTGTTTTTTTCGGCGGC......
                                                                                                                                                                             34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMet
                                                                                                                                                                                                                                                                               51 ValTrpAlaGlyIleAla...LeuLeuGlyLeuHisLeu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1213 CGCGCCGATCGTGCTCGATATTATGCGCTGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:

ID A52691 standard; DNA; 636 BF
XX A52691;
XX O3-JAN-2001 (first entry)
XX XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli yggA gene.
                         1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125
                                                                                                                                                                                                                                1121
                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA, isolated from Corynebacterium glutamicum, contains the LysG, LysE and ORF3 genes. LysG and LysE encode a lysine transport regulatory protein and an export protein. Respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.

NB. This sequence has been created from the information given in table 2
                                                                                                                                                                                                    LysG; LysE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing microbial production of amino acids, especially lysine by improving export carrier activity or corresponding gene expression, also new export and regulatory genes from
                                                                                                                                                    DNA encoding LysG, LysE and ORF3 from Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2374 BP; 526 A; 640 C; 648 G; 560 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 263
Gaps: 13
Percent Identity: 23.574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1723..2373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23 and 26; Page -; 16pp; German.
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
complement (82..954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ţ0;
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T96816 standard; DNA; 2374 BP
                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/label= LysG
1016..1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/label= LysE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/label= orf3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95DE-1048222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95DE-1048222
                                                                                                                                                                                                                                                                               Corynebacterium glutamicum
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108.00
0.900
45.627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the specification.
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US-09-466-935-4 x T96816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sahm H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-333867/31.
P-PSDB; W37714-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE19548222-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1995;
                                                                                                  12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eggeling L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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of L-amino acids by an Escherichia bacterium the expression amount of an L-amino acid excretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli; yfiK gene; amino acid production; excretion protein gene;
amino acid excretion protein; ds.
                                                                                               165 rValValAlaSerLeuPheAla.....LeuProGlnMetArgArgGly. 179
                                                                                                                                                               389 TIGTTGTACTGGGCAGCCTTGGGGGGCAACTTGATGTGGAACCAAAACGC 438
                                                                                                                                                                                                                                                                                                      150 TrpGlyIlePheAlaLeu...IleIleValGluThrLeuAlaTrpPheTh 165
                                                                                                                                                                                                                                                                                                                                                                                          483 TGGTCTGGCTCTTCTCGCTGCTGGCACCGCGTCTGCGCAA 532
                                                             254 TIGGCGCTITIAAAACAGCAAIGAGCAGTAATATIGAGTTAGCCAGCGCC 303
                                                                                                                                                                                         204 GCTGGCGCTGGTCACCTGGGGCGGCGTAGCCTTCTTGCTGTGGTATGGTT
                               87 yrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaProAla
                                                                                                                                                                                                                                    133 lySerValPheSerLeuPheValGlyAspAsnValGlyThrThrAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:A52690
                                                                                                                                                                                                                                                                                                                                                                                                                                           180 ..TyrGlnArgLeuAlaLysTrpIleAspGly 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 AAGCACAGCGCATTATCAATCTGGTTGTGGGA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..588
/*tag= a
/product= "Yfik"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 22; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99EP-0125263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98RU-0124016.
99RU-0104431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coll yfik gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID A52690 standard; DNA; 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increased production comprises increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-414802/36.
P-PSDB; B01788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Livshits VA,
Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1016710-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30~DEC-1998;
09~MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the yggA gene (an excretion protein gene) of Escherichia coil. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Increased production of L-amino acids by an Escherichia bacterium comprises increasing the expression amount of an L-amino acid excretion
                                                                                                                                                                                                                                                                                                                                                                           Troshin PV;
              E. coli; yggA gene; amino acid production; excretion protein gene; amino acid excretion protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 GlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLe 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 yProAspPhePhePalSerGlnThrAlaValSerArgSerArgLysG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 luAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAla 53
                                                                                                                                                                                                                                                                                                                                                                           Nakanishi K, Aleshin VV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....craccgcrcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 GGGATT.....TTTGGTGGCAGCGCGTTATTGATGCAGTCGCCGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 636 BP; 120 A; 143 C; 180 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 194
Gaps: 9
Percent Identity: 27.835
                                                                                                 Location/Qualifiers
1..636
/*tag= a
/product= "YggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 24; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 CTTGCACTTGGGGCGGCTATGATC.
                                                                                                                                                                                                                                                                                                                                                                           Zakataeva NP,
                                                                                                                                                                                                                                                       99EP-0125263
                                                                                                                                                                                                                                                                                       98RU-0124016
99RU-0104431
                                                                                                                                                                                                                                                                                                                                         AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103.00
1.030
51.546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: A52691
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US-09-466-935-4 x A52691
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-414802/36.
P-PSDB; B01789.
                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          rokhmakova IL;
                                                                                                                                                                                     EP1016710-A2
                                                                                                                                                                                                                                                                                       30-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                           Livshits VA,
                                                                                                                                                                                                                                                       17-DEC-1999;
                                                                                                                                                                                                                       05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                   Key
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52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu...... 62
31-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9428133-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hu S, Hu S, T D);
                                                                                                                                                                                                                                                                                                                  Ношо
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                           The present sequence is the yflK gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increased accumulation of amino acids in the cell. In this case, an increase in threonine, histidine, glutamic acid and proline is achieved if multiple copies of the gene are transfected into a bacterium. The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 leTyrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThr 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 TGTAC......GGTGTT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 GluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSerGlyAr 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 gSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 CAGCTTTTGGGCCAGCTTTGCTTTGTGAACGTCAAAATCATTT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 ThrAlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAlaTr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 GACGCCAGGACCGAACAATATTCTCGCCTTAGCTCTGCTACGTCGCATG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 ATTGTGATGTTACTGTGCGGGCATTTCA.....TTTTCACTGGC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 AGTGATTGACCCGGCAGCGGTACAC...CTTTTGAGTTGGGCGGGGGGGG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AAACCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 elleGluLysMetAlaTrpLeuHisThrLeulleMetValGlyGlyGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 CTTTTAAGTGCTTTTGGACTTACACC......CTGATTACCGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 euTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:Q80215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 erArgLysGluAlaMetMetGlyValLeuGlyIleThrCysGly.....
                                                                                                                                                                                                                                                                                   Sequence 588 BP; 113 A; 134 C; 167 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 22.034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 pPheThrValValAlaSerLeuPheAlaLeu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 GGTAGTTGGCGTCAGCGTTTTGCTGGCGATG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 GACGGACTTCAGGCA.....
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ID Q80215 standard; DNA; 1063 BP
                                                                                                                                                                                                                                                                                                                                                                                                       101.00
1.010
56.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: A52690
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Percent Similarity:
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factors (NDF's). The pertides encoded by these CDNA clones isolated from human tissues and cell lines, possess the ability to stimulate human pl8-neu tyrosine phosphorylation. These peptides have the ability to induce a differentiated phenotype in certain cell lines and can stimulate or inhibit proliferation of certain cell lines. The NDF's can be used to treat vounds, tumours derived from epithelial tissue of the breast, stomach etc., gastrointestinal disease, Barrett's ossophagus, (non-)oystic kidney disease or inflammatory bowel disease. These cDNA sequences may be used in a recombinant plasmid for the recombinant production of the NDF's in a pro- or eukaryotic host cell.
                                                      Alpha; beta; neu differentiation factor; NDF; human; rat; pl85-neu; ytyosine phosphorylation; differentiation; phenotype; proliferation; wound; tumour; epithelial tissue; breast; stomach; gastrointestinal disease; Barrett's oesophagus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences given in Q80215-22 encode human neu differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant neu differentiation factors and corresp. are used in the treatment of tumours, dermal wounds, and gastrointestinal, kidney and inflammatory bowel diseases.
                                                                                                                                                                     (non-)cystic kidney disease; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1063 BP; 291 A; 311 C; 246 G; 215 T; 0 other;
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Percent Identity: 27.919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugarman BJ;
                                                                                                                                                                                                                                                                                                                                                                           /product= Human NDF clone P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pierce GF,
                                                                                                                                                                                                                                                                               Location/Qualifiers
12..1055
/*tag= a
Human NDF-alphala clone P2 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-466-935-4 x Q80215/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1993;
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338

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represent the human ORFX open reading frames 1 to 3161. The ORFX represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiporvalatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiporvalant; antipartic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID). AIDS. viral, bacterial or fungal infection, malaria, autoimmune catiliage damage, nocturnal haemoglobinuria, antianiamatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 erPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIle 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 uAlaValSerAlaProAlaProGInValGluLeuAlaLysSerGlyArgS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 TyrPheGlySerValPheSerLeuPheValGlyAspAsnValGlyThrTh 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 401 BP; 57 A; 121 C; 124 G; 98 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 136
Gaps: 6
Percent Identity: 25.735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 607-608; 5507pp; English.
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31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127788.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540768.
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1.277
54.412
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                                                                                                                                                                                                   Leach M;
                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-466-935-4 x C74616
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                                                                                                                                                                                                                                                                WPI; 2000-6023
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                                                                                                                                                                                                      Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
      Human, open reading frame, ORPX, detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antionvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; que therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeflotency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal hæmoglobinuria; burn; wound; bone damage; oartilage damage; antiinflammatory disease; coaqulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 TATGGTCAGCACTCTCTTCTGGTACAGCTCCTCCGCCTCAATAAATTCAA 142
:::||| ::: ||| 457 CTGGTGGAAAGGATGTCTCTGCTTCTCTCTCTCAACAATATGCTCACTGGA 408
                                                                                                                                                                                                                                                                                                                                                                             112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ly.Thr.....ThralaArgTrpGlyIlePheAlaLeuIl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 ellevalGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euProGlnMetArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGly 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......AGATGCTTTCTTGGTTTTGGACT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF171 polynucleotide sequence SEQ ID NO:341.
                                                                                                                                             407 GATGACGTTTTTAGATACGTATTGATTCACCAGCTGGACATTCTCGGGGG
                                                                                                                                                                                                   78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL
                                                                                                                                                                                                                                             95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 Trcagacce.....aaggcrcrgccgaagac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GCCACCACACACATGATGCCGACCACAAGGAGGGCGATGCAGATGCCGGT
                                                                                   63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS2/gcgdata/geneseg/geneseqn/NA2000.DAT:C74616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 PheAlaGlyAlaLeuPheAlaGlyPheGlyIleHisLeu 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 TTCATGGGCACA.....TTCTCAGTACATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID C74616 standard; cDNA; 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 TCCCA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention decribes novel human nucleic acid sequences from tumor breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer. 233611-248617 represents expressed sequence tags described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosentahl A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human nucleic acid sequences and protein products from tumor breast
tissue, useful for breast cancer therapy –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tag; EST; human; breast; cancer; gene therapy; treatment; tumour; cytostatic; medicament; ss.
                                                                                                                                                               Dahl E,
                                                                                                        245 CGCTTGCAGTGTTTGTGCTGTATGGCCTGTTGGCGAATGTGTTT.....
                                                                    174 ProGlnMetArgArgGlyTyr.....GlnArgLeuAlaLysTrpIl
                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseg/geneseqn/NA1999.DAT:233622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (META-) METAGEN GES GENOMFORSCHUNG MBH.
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ID 233622 standard; cDNA; 1597
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                                                                                                                                                                                                                                                                      204 leserArg 206
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53 AlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMetAlaTr 69

from: 1 to: 1597

to: Z33622

Align seg 1/1

alignment\_block: US-09-466-935-4 x Z33622

Length: 180 Gaps: 11 Percent Identity: 27.778

90.50 1.077 46.667

Quality:
Ratio:
Percent Similarity:

236 136 137 TTAAGTACTICTGTTGCTGTTCTGTCATGAGTTGCCTCATGAATTAGG 186 ......ValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLeuL 120 SerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePh 153 eAlaLeuIleIleValGluThrLeuAlaTrpPheThrValValAlaSerL 170 ... ArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGl 192 86 lyTyrGlnMetLeuArgGlyAlaLeuLySLySGluAlaValSerAla... 101 419 AGCCGCTGGGGGTATTTTTTTTACAGAAT......GCTGG 453 92 21 pLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetG 86 GCCTAGCAATT.....GGTGCTGCTTTTACTGAAGGCTTATCAAGTGGT :: ::|||:::||| TTGATATGGTACCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGT TGACTITGCTGTTCTACTAAAGGCTGGCATGACCGTTAAGCAGGCTGTCC euThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerValPhe TGCACTT.....ACTGCTGGCTTATTCATGTTGTTGCTCTGG G.....Arggrgaraargggrgarggccrgcacaartrcagcgarg euPheAlaLeuProGlnMet,..... 

6.95

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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-847-743B-23 - 74.00 134.11 6.95 /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-456-201-23 - 74.00 134.11 6.95 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-456-201-33 - 74.00 134.11 6.95 /cgn2_6/ptodata/2/ina/FB_COMB.seq:PS-08-922-837-3 - 74.00 134.11 6.95 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-922-837-1 73.50 133.59 7.42
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                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-476-254-6
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Percent Identity: 25,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: WATSON COLE STEVENS DAVIS, P.L.L.C. STREET: 1400 K STREET NW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-476-254-6 from: 1
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NAME: POUTOS III. JAMES A.
REGISTRATION NUMBER: 31,714
REFERENCE/DOCKET NUMBER: JAP30319C
TELECOMUNICATION INFORMATION:
TELEPHONE: 202 628-0088
TELEPHAX: 202 628-0034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/476,254 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
; Sequence 6, Application US/08476254
; Patent No. 5846531
; GENERAL INFORMATION:
APPLICANT: WEINER, RONALD M.
APPLICANT: WOUGA, WILLIAM C.
; TITLE OF INVENTION: MARINE MELA GEN
; WINBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-09-466-935-4 x US-08-476-254-6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ropology:
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US-08-476-254-6
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                                                                                                                                                                                                                             Command line parameters:
-MODEL-frame+_L2D. incdel -DEV=xlp
-MODEL-frame+_L2D. incdel -DEV=xlp
-MODEL-frame+_L2D. incdel -DEV=xlp
-MODEL-frame+_L2D. incdel -DEV=xlp
-GFZTZ-1/USFTO.spool/US09466935/runat_03052001_075709_14814/app_query.fasta_1.529
-DE=ISsued_Patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=12.000
-GAPSTT-4.000 -MINATCH=-0.100 -LOOPEXT=0.000
-GAPSTT-4.000 -GAPEXT=0.050
-GAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS-human40.cdi -LIST=45 -DOCALIGN=2D0 -THR_SCORE-pct
-TRANS-human40.cdi -LIST=45 -DOCALIGN=2D0 -THR_SCORE-pct
-TRANS-human40.cdi -LIST=45 -DOCALIGN=0CAL -OUTFMT=pfs
-NONE=sxt -MINLEN-0 -MAXLEN-200000000
-USEN-SUS90466935_@CGN1_1_59 -NCFU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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76.50 131.70 9.06
74.00 134.40 6.69
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75.7 4.00 134.40 6.69
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                                                                                                                                                                  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
         out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/prodata/2/ina/5A_COMB.seq:US-08-096-277-6
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/cgn2_6/prodata/2/ina/5B_COMB.seq:US-08-612-734B-1 +
/cgn2_6/prodata/2/ina/5B_COMB.seq:US-08-612-734B-3 +
/cgn2_6/prodata/2/ina/5B_COMB.seq:US-08-612-734B-3 +
OM of: US-09-466-935-4 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
Query, US-09-466-933-4
Query length: 206
Database: Issued_Patents_NA:*
Database sequences: 302621
Database length: 87301344
Search time (sec): 80.320000
                                                                                     Date: May 6, 2001 3:40 PM
```

alignment_scores:     Quality: 107.00
seq_documentation_block: ;Patent No. 5474933 ;Patent No. 5474933 ;TILE OF INVENTION: MARINE MELA GENE ; NUMBER OF SEQUENCES: 9 ; CURRENT APPLICATION DATA; ; APPLICATION NUMBER: US/08/148,945 ;FILING DATE: 08-NOV-1993 ;PRIOR APPLICATION DATA: APPLICATION NUMBER: 974,837 ;FILING DATE: 10-NOV-1992 ;FILING DATE: 10-NOV-1992 ;APPLICATION NUMBER: 496,804 ;FILING DATE: 21-MAR-1990 ;SEQ ID NO:3: LENGTH: 720
 202 Leulleile 204     :::   FIGGCGCTA 705
 185 ystrpiledspGlyphealaGlyalaLeuphealaGlypheGlylleHis 201      ::::: :::        :::   ::   AGTGGATGAACCGCATAGCAGGAGTTTAATGATCGTGGTGGTTGGT
 175 nMetargargGlyTyrGlnArgLeualaL 185
 159 GluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeuProG1 175
 142 spAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLeuIleIleVal 158 ::: :: :: :: :: :: 516 TTGACCAAGCGATTGCAATTAATGGTATTACTGTCAATTATTAG 565
 125 nProLysAlaileileTyrPheGlySerValPheSerLeuPheValGlyA 142         ::   ## ## ## ## ## ## ## ## ## ## ## ## ##
 110 LysSerGlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAs 125     :::    ::::   :::       419AGTAATCGAGGCTAATAACTCAAGGCTTTGTCACCGGAATTGCTAA 465
 93 laLeuLysLysGluAlaValSerAlaProAlaProGlnValGluLeuAla 109
 76 1GlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyA 93 
60 LeuhisLeullelleGluLysMetAlaTrpLeuhisThrLeulleMetVa 76 ::: :::         :::::   278 GTCGCCAGTATGATGCTGCAACTATCCACAACTCTCGATATTTTAAAATG 327
 ::    :::     :::       :::

21 ProAsphePhePheValserG  118 CCGACCTTTTTTTCGTCTCAA  30AlavalserArg  43 euGlylleThrCyGGTATGGTATCG  43 euGlylleThrCyGGTATGGTTGC  60 LeuHisLeuIleIluLysm  118 CTGCCAGTATGACTGGTACTG  51
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m

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seq_documentation_block:
    Sequence 7, Application Us/08096277
    Sequence 7, Application Us/08096277
    Patent No. 5578482
    GENERAL INFORMATION:
    APPLICANT: Lippman, Marc E
    APPLICANT: Lippman, Marc E
    TITLE OF INVENTION: Ligand Growth Factors that Bind to the
    TITLE OF INVENTION: erbB-2 Receptor Protein and Induce Cellular Response
    NUMBER OF SEQUENCES: 18
    CORRESPONDENCE ADDRESS:
                                                                                                                                                   845 TATGGTCAGCACTCTCTTCTGGTACAGCTCCTCCGCCTCCATAAATTCAA 796
145 ly.Thr.....ThrAlaArgTrpGlyIlePheAlaLeuIl 156
                                                                                                                     156 ellevalGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173
                                                                                                                                                                                                                                           173 euProGlnMetArg......177
                                                                                                                                                                                                                                                                                                      795 ICCCAAGAIGCIIGIAGAAGCIGGCCAIIACGIAGIITIIGGCAGCGAICA 746
                                   || || || || 895 GCCACCACACACATGCCGACCACCACATGCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-096-277-7
                                                                                                                                                                                                                                                                                                                                                                                                 745 CCAGTAAACTCATTTGGGCACTTGCACAAGTATCTCGAGGGTTT 701
                                                                                                                                                                                                                                                                                                                                                             178 .....ArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Banner, Birch, McKie & Beckeet STREET: 1001 G Street, N.W. CITY: Washington STATE: D.C. COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/096,277
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/875,788
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/640,497
FILING DATE: 14-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,988
FILING DATE: 24-JUL-1992
PRIOR APPLICATION NUMBER: US 07/917,988
FILING DATE: 24-JUL-1992
PRIOR APPLICATION NUMBER: US 07/872,114
FILING DATE: 22-APR-1992
FILING DATE: 22-APR-1993
FILING DATE: 22-APR-1993
FILING DATE: 22-APR-1993
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 07/528,438
FILING DATE: 25-MAY-1990
ATTORNEY ARGAIT INFORMATION:
NAME: US-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02899.43360
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TELEPHONE: 202-508-9100
TELEPA: 202-508-9299
TELEX: 197430 BBMB UT
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2199 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hoscheit, Dale H
REGISTRATION NUMBER: 19,090
REFERENCE/DOCKET NUMBER: 028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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1061 GATGACGTTTTTAGATACGTATTGATTCACCAGCTGGACATTCTCGGGGG 1012 1152 GGGTGACAGT...AGTGGAGTGATGGGC......TGTGGAAGTATAGTGA 1112 ::|||::: 795 TCCCAAGATGCTTGTAGAAGCTGGCCATTACGTAGTTTTGGCAGCGATCA 746 112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128 128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145 936 GGTCATG ......CAGCTPTTTCCCTGTTTCTTGCAGTAG 896 145 ly.Thr.....ThrAlaArgTrpGlyIlePheAlaLeuIl 156 895 GCCACCACACACATGATGCCGACCACAAGGAGGCGCATGCAGATGCCGGT 846 845 TATGGTCAGCACTCTTCTGGTACAGCTCCTCCGCCTCCATAAATTCAA 796 95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 111 992 ......CCCATIGGCAAIGTTCATCATATIGTTTCG 963 962 ITCAGACCG.............AAGGCICTGCCGAAGAC 937 elleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173 20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35 35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT 52 63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl 78 78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL 95 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-456-201-7 APPLICANT: Vandlen, Richard L.,
APPLICANT: Vandlen, Richard L.,
APPLICANT: Vandlen, William E.
TITLE OF INVENTION: Structure, Production and Use of
TITLE OF INVENTION: Herequiin 2 Ligands
CORRESPONDENCE ADDRESS: 178 .....ArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190 745 CCAGTAAACTCATTTGGGCACTTGCACAAGTATCTCGAGGGGTTT 701 Align seg 1/1 to reverse of: US-08-096-277-7 from: 1 Length: 199 Gaps: 12 Percent Identity: 26.131 52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu..... alignment\_block: US-09-466-935-4 x US-08-096-277-7/rev seq\_documentation\_block:
; Sequence 7, Application US/08456201; Patent No. 5641869
; GENERAL INFORMATION: 173 euProGlnMetArg..... 90.00 0.938 48.241 alignment\_scores: Quality: Ratio: Percent Similarity: US-08-096-277-7 156

Align seg 1/1 to reverse of: US-08-456-201-7 from: 1 to: 2199 1111 CTGGTGGAAAAGGATGTCTCTCTCTCTCTCAACAATATGCTCACTGGA 1062 1061 GATGACGTTTTTAGATACGTATTGATTCACCAGCTGGACATTCTCGGGGG 1012 95 ysLysGluAlaValSerAlaProAlaProGlnValGluLeuAlaLysSer 111 20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35 35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT 52 95 63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl 78 78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL Length: 199 Gaps: 12 Percent Identity: 26.131 52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu...... COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
FILING DATE:
APPLICATION NUMBER: U7/080,917
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/70526
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/790801
ATTORNEY AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 712P4
REFERENCE/DOCKET NUMBER: 712P4
TELECOMMUNICATION INFORMATION:
TELECHOME: 415/266-1489 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201 ADDRESSEE: Genentech, Inc. TyreEr: 460 Point San Bruno Blvd CITY: South San Francisco STATE: Callfornia alignment\_block: US-09-466-935-4 x US-08-456-201-7/rev TELEFAX: 415/952-9881 TELEX: 910/371-7168 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single 2199 bases USA Quality: Ratio: Percent Similarity: 94080 alignment\_scores: COUNTRY: LENGIH:

	156 ellevaloluThrLeualaTrpPheThrValValAlaSerLeupheAlaL 173 ::::   ::	Seq_documentation_block: Sequence_7, Appl_cation_US/08456241 Sequence_7, Appl_cation_US/08456241 Relear No. 58405_5 GENERAL INFORMATION: APPLICANT: Vandlen, Richard L. APPLICANT: Vandlen, Richard L. APLICANT: Wandlen, Richard L. TITLE OF INVENTION: STROCTURE, PRODUCTION AND USE OF TITLE OF INVENTION: BREGGILIN NUMBER OF ESQUENCES: S CORRESPONDENCE ADDRESS: ADDRESSEE: Generace, Inc. STREET: 460 Point San Bruno Blvd STATE: Callfornia CIP: South San Francisco STATE: Callfornia CIP: State: As Compatible APPLICATION NUMBER: 07/44773 APPLICATION NUMBER: 07/4779801 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: CIP: State: OF COMPATION DATA: APPLICATION NUMBER: 07/75212 PRIOR APPLICATION NUMBER: 07/75212 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/75212 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/75212 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/75212 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/75212 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/75212 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/75212 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/75212
	156 e11eValG 173 euProGln 173 euProGln 795 rCCCAAGA 178Ar 745 CCAGTAAA 8eg_name: /cgn2_6	Seq_documentation Sequence 7, App Patent No. 5840 GENERAL INFORM APPLICANT: TITLE OF INV TITLE

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Align seg 1/1 to reverse of: US-08-456-241-7 from: 1 to: 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1152 GGGTGACAGT...AGTGGAGTGATGGGC.....TGTGGAAGTATAGTGA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1061 GATGACGTTTTTAGAFACGTATTGATTCACCAGCTGGACATTCTCGGGGG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1111 CTGGTGGAAAAGGATGTCTCTGTCTCTCTCAACAATATGCTCACTGGA 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  795 TCCCAAGATGCTTGTAGAAGCTGGCCATTACGTAGTTTTGGCAGCGATCA 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        962 TTCAGACCG............AAGGCTCTGCCGAAGAC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 euProGlnMetArg......177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT 52
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Gaps: 12
Percent Identity: 26.131
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00.000
REFERENCE/DOCKET NUMBER: 712P4C1D1
TELECOMMUNICATION INFORMATION:
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US-09-466-935-4 x US-08-456-241-7/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 90.00
Ratio: 0.938
Percent Similarity: 48.241
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20 GlyProAspPhePhePheValSer...GlnThrAlaValSerArgSerAr 35
                                                                                      Agreence 7, Application US/08550815
Patent No. 5865618
Patent No. 5865618
GENERAL INFORMATION:
APPLICANT: Lippman, Marc E
APPLICANT: Lippman, Marc E
APPLICANT: Lippman, Ruth
TITLE OF INVENTION: Ligand Growth Factors that Bind to the
TITLE OF INVENTION: Ligand Growth Factors that Bind to the
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckeet
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 2199
                      seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-550-815-7
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Gaps: 12
Percent Identity: 26.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/550,815
FILING DATE: 31-OCT-1995
CLASSIFICATION: 536
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PRIOR APPLICATION NAMBER: US 08/096,277
FILING DATE: 29-67-1992
PRIOR APPLICATION NUMBER: US 07/875,788
FILING DATE: 29-67-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/640,497
FILING DATE: 14-70A-1991
PRIOR APPLICATION NUMBER: US 07/917,988
FILING DATE: 24-JUL-1992
PRIOR APPLICATION NUMBER: US 07/872,114
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,114
FILING DATE: 22-APR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA: 22-APR-1992
FILING DATE: 22-APR-1992
APPLICATION DATA: 32-APR-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-466-935-4 x US-08-550-815-7/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hoscheit, Dale H
RECISTRATION NUMBER: 19,090
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202-508-9299
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0.938
48.241
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MEDIUM TYPE: Floppy
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                                                                      seq_documentation_block
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-08-550-815-7
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seq_documentation_block:
    Sequence 7. Application US/08703089
    Sequence 7. Application US/08703089
    General No. 6040390
    General Information:
    Applicant: Lippman, Marc E
    Applicant: Lippman, Marc E
    TITLE OF INVENTION: Lipand Growth Factors that Bind to the
    TITLE OF INVENTION: erbB-2 Receptor Protein and Induce Cellular Response
    NUMBER OF SEQUENCES:
    CORRESPONDENCE ADDRESS:
128 allelleTyrPheGlySerValPheSerLeuPheValGlyAspAsnValG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 ly.Thr......ThralaArgTrpGlyIlePheAlaLeuIl 156
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                                                                      35 gLysGluAlaMetMetGlyValLeuGlyIleThrCysGlyValMetValT 52
                                                                                                                                                                           52 rpAlaGlyIleAlaLeuLeuGlyLeuHisLeu......... 62
                                                                                                                                                                                                                                                                                                                                                                               78 yGlyLeuTyrLeuCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....CCCATTGGCAATGTTCATATTGTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl
                                                                                                                                                                                                                                                                             63 ...IleIleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 ..... ArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            745 CCAGTAAACTCATTTGGGCACTTGCACAAGTATCTCGAGGGTTT 701
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Banner, Birch, McKie & Beckeet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1001 G Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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seq\_name: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:PCT-US92-04295A-7 ::::::: CAGCTTTTTCCCTGTTTTTCCAGTAG 896 .....ThrAlaArgTrpGlyIlePheAlaLeuIl 156 895 GCCACCACACATGATGCCGACCACAAGGAGGGCGATGCAGATGCCGGT 846 845 TATGGTCAGCACTCTCTCTGGTACAGCTCCTCCGCCTCCATAAATTCAA 796 156 eIleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaL 173 173 euProGlnMetArg......177 795 ICCCAAGAIGCIIGIAGAAGCIGGCCAIIACGIAGIIIIGGCAGCGAICA 746 128 allerleryrPheGlySerValPheSerLeuPheValGlyAspAsnValG :::::::: seq\_documentation\_block:
 Sequence 7, Application PC/TUS9204295A
 GENERAL INFORMATION:
 TILE OF INVENTION: Structure, Production and Use of TILE OF INVENTION: Herequlin
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS: 178 .....ArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPhe 190 145 CCAGTAAACTCATTTGGGCACTTGCACAAGTATCTCGAGGGGTTT 701 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19920521
\*RIOR APPTICATION: STREE: Genericch, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California CONTRY: USA PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/847743
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION: NAME: Hensley Max D. REGISTRATION NOMBER: 27,043
REFERENCE/DOCKET NUMBER: 711
TELECHONE: 415/225-1994
TELEFAX: 415/292-1994 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 2199 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: linear 145 ly.Thr..... 962 ITCAGACCG...

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Align seg 1/1 to reverse of: US-08-390-878-17 from: 1 to: 15239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 rProGlyProAspPhePhePheValSerGlnThrAlaValSerArgSerA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSe 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 TrpAlaGlyIle......AlaLeuLeuGlyLeuHisLeuIleIl
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                                                                                                                               JETE 94105

JETE: 94105

JETE: 94105

MEDIUM TYPE: Floppy disk

COMPUTER: TEM FC compatible

COMPUTER: TEM FC compatible

COMPUTER: TEM FC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,878

FILING DATE: 17-FEB-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HUNCEY. TON

NAME: HUNCEY. TON

NAME: HUNCEY. TON

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 415/43/9600

TELEFAX: 415/43/9600

TELEFAX: 415/43/9600

TELEFAX: 415/43/9600

TELEFAX: 415/43/9600

TELEFAX: 415/39/960

TELEFAX: 415/39/960

TELEFAX: 415/39/960

TELEFAX: 415/39/960

TELEFAX: 415/39/960

TENGTH: 1539 base pairs

TVPE: ULOCHOLOGY: Linear

MOLECULE TYPE: DNA (GENOMIC)

US-08-390-878-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 11
Percent Identity: 22.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5090 CIGGCCIGCTICACGCIGAICGCCGCGAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-466-935-4 x US-08-390-878-17/rev
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51.613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.00
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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seq_documentation_block:
; Sequence 1, Application Us/08311023
; Patent No. 5693465
; Fatent No. 5693465
; Fatent InFORMATION:
APPLICANT: MANNING, David Lockwood
APPLICANT: NICHOLSON, Robert Ian
APPLICANT: GREEN, Christopher Douglas
; TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: METHODS OF
STATE: 745 South 23rd Street
CITY: Arlington
STATE: VA
COUNTY: USA
ZIP: 22202
COMPUTER PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                          4621 GCCGGTTGCGCGGGCTGTTCACCAACCCCGGCTGGAGATCCTCGAC 4572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 roGlnMetArgArgGlyTyrGlnArgLeuAlaLysTrp.....IleAsp 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 GlyPheAlaGlyAlaLeuPheAlaGlyPheGlyIleHisLeuIleIleSe 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Detenting states and states are supplied to the states and states are supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to the supplied to th
                                                                                                                                                                                                                                                                                                                                                                                 157 eValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheAlaLeuP 174
125 snProLysAlaIleIleTyrPheGlySerValPheSerLeuPheValGly 141
                                                                                                                                                                                142 AspAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLeu...IleIl
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INPOMENTION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1310 base pairs
TYPE: nucleic acid
STRANDEDMESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08~311-023-1
```

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seq_documentation_block:
; Sequence 3, Application US/08311023
; Patent No. 5693465
; GENERAL INFORMATION:
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: MICHOLSON, Robert Ian
APPLICANT: GREEN, CHIES CON REPLICANT:
TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
TITLE OF INVENTION: BREAST TUMOURS
NUMBER OF SEQUENCES:
ADDRESSEE: YOUNG & Thompson
STREET: 745 South 23rd Street
CITY: Alington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: ::||||:::||||
1127 TIGATATGGTACCTGAAATGCTGATGATGTGATGTGACCATGGATGT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 G.....ATGGTGATAATGGGTGATGGCCTGCACAATTTCAGCGATG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                    106 ......valGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLeuL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerValPhe 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 SerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePh 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 eAlaLeuIleIleValGluThrLeuAlaTrpPheThrValValAlaSerL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 ... ArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGl 192
                                                                                                                                                                                                                                                                    787 GCCGGCGTCGCCACTTTG.....GCCTG 809
                                                                                                                                                                                                                                                                                                                                                                                                           86 lyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSerAla... 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            895 TTAAGTACTTCTGTTGCTGTTTCTGTCATGAGTTGCCTCATGAATTAGG 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    945 TGACTTTGCTGTTCTACTAAAGGCTGGCATGACCGTTAAGCAGGCTGTCC 994
                                                                                                                                                                                                                         53 AlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMetAlaTr 69
                                                                                                                                                                                                                                                                                                                  69 pLeuHisThrLeuIleMetValGlyGlyGlyLeuTyrLeuCysTrpMetG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 ......ProAlaProGln.....
                    Length: 179
Gaps: 11
Percent Identity: 27.374
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                                                                                                                                                                              from: 1
                                                                                                                                                                            Align seg 1/1 to: US-08-311-023-1
                                                                                                            alignment_block:
US-09-466-935-4 x US-08-311-023-1
                    86.50
1.042
46.369
                                             Ratio:
Percent Similarity:
                      Quality:
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170
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COMPUTER READABLE FORM:
MEDIUT TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,023
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: WEG. NO. 5693465 32,925
REFERENCE/DOCKET NUMBER: WCM.56
TELECOMMULCATION NUMBER: WCM.56
TELECOMMULCATION INFORMATION:
TELEPHONE: 703/521-2297
TELEFRAX: 703/685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 eAlaLeuIleIleValGluThrLeuAlaTrpPheThrValValAlaSerL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euPheAlaLeuProGlnMet......176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 ......105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         945 IGACTTTGCTGTTCTAAAGGCTGGCATGACGTTAAGCAGGCTGTCC 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 euThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerValPhe 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePh 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AlaGlylleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895 TTAAGTACTTCTGTTGCTGTTTCTGTCATGAGTTGCCTCATGAATTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 179
Gaps: 11
Percent Identity: 27.374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-311-023-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-466-935-4 x US-08-311-023-3
                                                                                                                                                                                                                                                                                                   TELEX: 248425
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.50
1.042
46.369
                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: CDNA US-08-311-023-3
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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1177 AGCCGCTGGGGGTATTTCTTTTACAGAAT......GCTGG 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::::||||||| ::::::|||| 3347 createrecationalecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecaterecatereca
177 ... ArgArgGlyTyrGlnArgLeuAlaLysTrpIleAspGlyPheAlaGl 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1. Application US/08395246C

Patent No. 577314

GENERAL INFORMATION:
APPLICANT: Peery, Robert B.
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF TITLE OF INVENTION: ASPERGILLUS FLAVUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 MetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerPr 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 oGlyProAspPhePhePheValSerGlnThrAlaValSerArgSerArgL 36
                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-395-246C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 4355
CLASSIFICATION: 4355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 8
Percent Identity: 23.699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-395-246C-1 from: 1 to: 3924
                                                                                                                                                                                                                                                                                      1212 GATGCTTTTG...GGTTTTGGAATTATGTTACTTATT 1245
                                                                                                                                                                                                         192 yAlaLeuPheAlaGlyPheGlyIleHisLeuIleIle 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35784
REFERENCE/DOCKET NUMBER: x96(
TELE/DOWINIACTION INFORMATION:
TELERAN: 317-276-2459
TELERAN: 317-277-1917
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3924 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-466-935-4 x US-08-395-246C-1
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 85.50
Ratio: 1.082
Percent Similarity: 45.665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
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; LOCATION:
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seq_documentation_block:
    Sequence 1, Application US/09335409
    Patent No. 6121029
    General Information:
    APPLICANT: Schupp, Thomas
    APPLICANT: Ligon, James
    APPLICANT: Like, Ross
    APPLICANT: Girkle, Ross
    APPLICANT: Girkle, Ross
    APPLICANT: Gyr, Devon
    APPLICANT: Gyr, Devon
    APPLICANT: Gyr, Devon
    APPLICANT: Gyr, Devon
    APPLICANT: Gorlach, Joern
    TITLE OF INVENTION: Genes FOR THE BIOSYNTHESIS OF EPOTHILONES
    CURRENT APPLICATION NUMBER: US/09/335,409
    CURRENT FILING DATE: 1999-06-17
    WUMBER OF SEQ ID NOS: 30
    SOFTWARE: PatentIn Ver. 2.0
    SEQ ID NO 1
    LENGTH 68750
                                                                                                                                                                                                                                                    2596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2497 CAGGAAAACACGACAGGGGGATTAACAGCCACTCTGAGCGGGGGGGCCAA 2546
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                                                                                                                                                                                              39 ....MetMetGlyValLeuGlyIleThrCysGlyValMetValTrpAlaG
::: |||::: |||::: |||| |||::: ||||
2547 AGAACTAACTGGCATTAGTGGCGTCACATTGGGGACTATCTGTTGATGTCT
                                                                                                                                                                                                                                                                                                 54 ly......IleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                       2638 GGCTGGAAGTTGGCACTGGTGCATCTCGCGGGTTCCAGCCTGGTGAT
                                                                                                                                                                                                                                                                                                                                    82 uCys......TrpMetGlyTyrGlnMetLeuArgGlyAlaL
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Gaps: 9
Percent Identity: 22.010
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36 ysGluAla......
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; ORGANISM: Sorangium cellulosum
US-09-335-409-1
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1 MetLeuMetLeuPheLeuThrValAlaMetValHisIleValAlaLeuMe 17

APPLICANT: BOTHER, William S.
APPLICANT: CANDER, William S.
APPLICANT: CANDER, MAIN P.
APPLICANT: CANDER, MAIN V.
APPLICANT: METEZ, James R.
TITLE OF INVENTION: POTENT INHIBITORS OF HUMAN 9-cis RETINOL DEHYDROGENASE FILE REFERENCE: 0575/54544
CURRENT APPLICATION NUMBER: 0576/940, 424A
CURRENT FILING DATE: 1997-09-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 10 3831 GATCGTGCTCTCGGTGACGGCGGTCAGCGTGATCGCGAAGGTGCTGATCG 3880 .........GGCCTCTTCCTCGG 3830 105 nValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLeuLeuThrA 122 139 PheValGlyAspAsnValGlyThrThrAlaArgTrpGlyIlePheAlaLe 155 155 ullelleValGluThrLeuAlaTrpPheThrValValAlaSerLeuPheA 172 89 MetLeuArgGlyAlaLeuLysLysGluAlaValSerAlaProAlaProGl 105 hrLeulleMetValGlyGlyGlyLeuTyrLeuCysTrpMetGlyTyrGln 88 17 tSerProGlyProAspPhePhePheValSerGlnThrAlaValSerArgS 34 seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:US-08-940-424-10 122 snLeuAlaAsnProLysAlaIleIleTyrPheGlySerValPheSerLeu 3609 CCAGGAGCCGGCGGTCGGGGTCGTCTCGGGCCATCTCCTGG...... 34 erArgLysGluAlaMetMetGlyValLeu.....GlyIleThrCysGly 49 ValMetValTrpAlaGlyIleAlaLeuLeuGlyLeuHis..... 3691 GTCGACGTGGGCATCCTGCGCAAGGAGGCG 3931 GTGGTCAGCGAGGTCGCTGCCTGGGTG 3957 172 laLeuProGlnMetArgArgGlyTyr..... 181 .....GlnArgLeuAlaLysTrpile 187 seq\_documentation\_block:
 Sequence 10, Application US/08940424A
 Patent No. 6171837
 Sequence No. 6171837 3790 credrecrearcescerrecase. ; TYPE: DNA ; ORGANISM: mouse US-08-940-424-10 3487

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136 heSerLeuPheValGlyAspAsnValGlyThrThrAlaArgTrp..... 150
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                                                                                                                                                                                                                                                                                                                                                                                                                            103 AlaProGlnValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyLe 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 uLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerValP 136
                                                                                                                                                                         28 nThralaValSerArgSerArgLysGlualaMetMetGlyValLeuGlyI 45
                                                                                                                                                                                                                                                                           45 leThrCysGlyValMetValTrpAlaGlyIleAlaLeuLeuGlyLeuHis 61
                                                                                                                                                                                                                                                                                                                                                                                                      78 y.....GlyLeuTyrLeuCysTrpMetG 86
                                                                                                                                                        12 HisileValAlaLeuMetSerProGlyProAspPhePheValSerGl 28
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Gaps: 9
Percent Identity: 22.488
                                                                                                                      Align seg 1/1 to: US-08-940-424-10 from: 1 to: 1229
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US-09-466-935-4 x US-08-940-424-10
alignment_scores:
   Quality:
   Ratio:
   Percent Similarity:
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May 6, 2001, 14:40:01; Search time 26.05 Seconds (without alignments) 543.452 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 ~ 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1054
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

PIR\_67:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT F64115

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119.5	119	10	10	ĭ	Н	٦			6	95			92		

## ALIGNMENTS

	hypothetical 13.3 KD protein in recQ 3' region - Escherichia coli (strain K-12) NAlternate names: hypothetical protein ol28	a coli (strain K-12)
	C; Species: Escherinia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999	ange 08-Oct-1999
	R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,	.; Burland, V.; Riley, M.,
	.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997	
	A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617	-12.
	A,Accession: B65186	
_	A; Molecule type: DNA  A; Molecule type: DNA	istation not shown
	A; Residues: 1-122 <blat></blat>	
	A. CLOSS-Treferences: GB-AE0004648; GB-U00096; NID:92367299; PIDN:ARC76826.1; PID:923673	IDN:AAC76826.1; PID:923673
	A. Larket Himmilian Doutce: Strain R. L., Substant Maileon R. Daniels D. L. : Plunkett III. G. Rurland V : Rlattner F R	Ω
	Aprile: Analysis of the Bscherionia coli genome: DNA sequence of the region from	ice of the region from 84.
	A; Releterence number: 550500; MOLD:92556234	
	A, Status: preliminary; nucleic acid sequence not shown; translation not	nslation not shown
	A; Molecule type: DNA	
	A; Residues: 'VAVSLLD', 2, 'LPDATWCTE', 12, 'RGGFCTCATGRAGEKWAQ', 31, 'PES', 35-122 <dan></dan>	,31,'PES',35-122 <dan></dan>
	A;Cross-references: EMBL:M87049	
	A; Note: this sequence has been corrected	
	A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992	ita Library, November 1992
	A;Gene: ½1gJ	
	Ouery Match 58.6%: Score 618: DB 2: Length 122:	122;
	Similarity 100.0%; Pred. No. 2.6e-48; 2; Conservative 0; Mismatches 0;	
	Qy 85 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNV	SVFSLFVGDNV 144
	DD 1 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNV	
	Qy 145 GTTARWGIFALIIVETLAWFTVVASLFALPOMRRGYORLAKWIDGFAGALFAGFGIHLII	SEAGEGIHLII 204
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	DD 61 GTTARMGIFALIIVETLAWFTVVASLFALÞQMRRGYQRLAKWIDGFAGALFAGFGIHL	FAGFGIHLII 120
	Oy 205 SR 206	
	Db 121 SR 122	
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hypothetical protein BH2932 (imported) - Bacillus halodurans (strain C-125)
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Accession: D84016
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A; Reference number: A83650; MUID:20263314
A; Reference number: A83650; MUID:20263314
A; Recension: D84016
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-210 <STC>
A; Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06651.1; GSPDB:G
C; Genetios:
A; Gene: BH2932
C; Superfamily: hypothetical protein b1798
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Status: 204 <25TO>
A;Status: STTO>
A;Ctoss-references: GB.AE004719; GB.AE004091; NID:g9949021; PIDN:AAG06317.1; GSPDB:GN
A;Experimental source: strain PA01
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A.; Larbig,
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                                                          64 YLVKQQPMLFNLLQLAGGSYLLYLGAGALQSVWAQKNASTPFHSPAPSI-LGNRRQAFTK 122
                                                                                                                                                    GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                  GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
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                       62 LIIEKMAWLHTLIMVGGLYLCWMGYQMLRGALKKEAVS--
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Matches 67,
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C;Species: Yibrio cholerae
C;Gate: 18 Aug-2000 fsequence_revision 20-Aug-2000 ftext_change 15-Sep-2000
C;Accession: P83253
B;Heidelberg, J.F.: Eisen, J.A.; Nelson, W.C.; Bass, S.; Qin, H.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Draggi, I.; Sellers, F
J. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Mature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD:20406833
A;Actus: preliminary
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-222 < HEL>
A;Cross-references: GB:AE004109; GB:AE003852; NID:g9654590; PIDN:AAF93367.1; GSPDB:GN001
A;Edenetics: VOGIG: A;Genetics: VOGI
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hypothetical protein H11307 - Haemophilus influenzae (strain Rd KW20)
C;Species: Raemophilus influenzae
C;Oate : 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C;Accession: F64115
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R.; Gocayne, J.D.; Schirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weldman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Genem, C.E., McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A6400; MUID:95350630
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-210 <TIGR>
A;Cross-references: GB:U32810; GB:L42023; NID:g1574760; PIDN:AAC22954.1; PID:g1574766; R.C.; Chentics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKS---GRSFLKGLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TNLANPKAIIYFGSVFSLFVGDNVGTTARWGI----FALIIVETLAWFTVVASLFALPQMR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI 63
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Pred. No. 6.9e-21;
2; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 368.5; DB 2
Pred. No. 8.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Start codon: GTG
C;Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 RGYQRLAKWIDGFAGALFAGFGIHLI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.7%; Scc
Best Local Similarity 31.3%; Pre
Matches 62; Conservative 52;
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38.8%;
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Best Local Si
Matches 80;
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C;Species: Escherichia coli
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C;Species: Escherichia coli
C;Species: H44759
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.R.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; And, B.; Shao, Y.
A;Ritle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MuID:97426617
A;Reference number: A64720; MuID:97426617
A;Reference number: A64720; MuID:97426617
A;Reference number: A64720; MuID:97426617
A;Reference number: BNA
A;Residues: 1-223 <BLAT>
A;Residues: 1-223 <BLAT>
A;Residues: 1-223 <BLAT>
A;Residues: 1-223 <BLAT>
A;Reperimental source: strain K-12, substrain MG1655
C;Genetics:
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A Status: preliminary
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A Status:
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: F8344  
E;Accession: F83444  
E;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; I. Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID: 20437337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 PWLRGVATNLFNPKALVFFIALLGSLIPAQMSLGGKLAVAALLFGMGACWFGLLSLTLTR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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24.8%; Score 261.5; DB 2; Length 223;
Best Local Similarity 28.2%; Pred. No. 3e-16;
Matches 58; Conservative 50; Mismatches 83; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 213;
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C;Superfamily: hypothetical protein b1798
C;Keywords: transmembrane protein
F;26-42/Domain: transmembrane #status predicted <TM1>
F;26-101/Domain: transmembrane #status predicted <TM2>
F;16-179/Domain: transmembrane #status predicted <TM3>
F;16-179/Domain: transmembrane #status predicted <TM3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 25.0%; Score 263.5; DB 2;
Local Similarity 27.3%; Pred. No. 1.9e-16;
Les 59; Conservative 46; Mismatches 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 POMRRGYQRLAKWIDGFAGALF ---- AGFGIHLIIS 205
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Best Local S
Matches 59
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Cippecies: Versinia enterocolitica
Cippecies: Versinia enterocolitica
Cipacession: T4321
Risaken, E.M.: Rakin, A.V.: Heesemann, J.
Submitted to the EMBL Data Library, November 1999
Albestiption: Molecular characterization of a novel siderophore-independent iron transf
Albestiption: Molecular characterization of a novel siderophore-independent iron transf
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F88444
hypothetical protein PA1620 [imported] - Pseudomonas aeruginosa (strain PAOI)
C;Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 VLVRESLALFTALKLAGAAYLVFLGLRML--LAREDSVAEEAAGGAGVSWAMLRSGFLT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQ 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHL 62
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                                                                                                                                                                                                                                                                                                                                                                                      2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                                                                                                       Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 212;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                              ; Score 274.5; DB 2;
; Pred. No. 1.9e-17;
42; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 269.5; DB : Pred. No. 5.6e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POMRRGYQRLAKWIDGFAGALFAGFGIHLI 203
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    C;Genetics:
A;Gene: PA2929
C;Superfamily: hypothetical protein b1798
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A,Gene: yfub
C,Superfamily: hypothetical protein b1798
C,Keywords: iron transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 RLAKWIDGFAGALFAGFGIHL 202
                                                                                                                                                                                                              26.0%;
ilarity 32.3%;
Conservative 4:
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Best Local Similarity 28.1%;
Matches 59; Conservative 5
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 65; Conserv
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"Upportherical protein PA5341 [imported] - Pseudomonas aeruginosa (strain PAO1)
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
R.Stover, C.K.; Phan, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
R.Stover, C.K.; Phan, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
I.Ory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A.Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A.Title: Type: DN
A.Tocossion: C82979
A.Status: preliminary
A.Accession: C82979
A.Status: Preliminary
A.Rociecule type: DN
A.Rociecule type: DN
A.Rociecule (SPO)
A.Tocos references: GB:RE004946; GB:AE004091, NID:99951650; PIDN:AAG08726.1; GSPDB:GN
A.Experimental source: strain PAO1
A; Molecule type: DNA
A; Residues 1.210 - GST.O-
A; Residues 1.210 - GST.O-
A; Cross-references: GSTAE004864; GB: AE004091; NID: 99950740; PIDN: AAG07895.1; GSPDB: GN
A; Experimental source: strain PAO1
A; Experimental source: strain PAO1
A; Genetics:
A; Genetics:
C; Genetics: PA4507
C; Superfamily: hypothetical protein b1798
                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASL----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 LIVLGLLASVPDSAHSALRWLQAL----GGLYFLWLAGQAL---LAQRRLEMPAQRDVPS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSG--RSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTAR-----WGI---FALIIVE 159
                                                                                                                                                                                                                                                                                                                                                                                            6 LIVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGI----TCGVMVWAGIALLGLH 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 206;
                                                                                                                                                                                                                                          Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match

19.8%; Score 208.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 1.5e-11;
Matches 65; Conservative 32; Mismatches 86;
                                                                                                                                                                                                                                          Ouery Match 23.2%; Score 245; DB 2; Best Local Similarity 33.3%; Pred. No. 8.4e-15; Matches 75; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PA5341
C;Superfamily: hypothetical protein b1798
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C; Specias: Pseudomonas aeruginosa
C; Specias: Pseudomonas aeruginosa
C; Specias: Pseudomonas aeruginosa
C; Specias: Pseudomonas aeruginosa
C; Specias: Pseudomonas aeruginosa
C; Specias: Pseudomonas aeruginosa
C; Specias: Pseudomonas aeruginosa
C; Specias: Pseudomonas aeruginosa
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
Adcression: Rs3306
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor
A; Reference number: A82950; MUID: 20437337
A; Reference number: A82950; MUID: 20437337
A; Molecule type: DNA
A; Residues: DNA
A; Residues: 1-204
A; Residues: 1-204
A; Residues: 1-204
A; Residues: Strain PA01
C; Genetics: Pa2710
C; Superfamily: hypothetical protein b1798
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() Species: Pseudomonas aeruginosa

() Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

() Accession: 639082

R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, A.L., A.S., A.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathod A.Recession: 683082

A; Stetus: preliminary
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                                                                                       64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRS-----FLK 117
                                                                                                                                                        118 GLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
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   VYLTVGL-FVITFFNPGANLFVVVQTSLASGRRAGVLTGLGVALGDAFYSGLGLFGLATL 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 POMRRGYORLAKWIDGFAGALFAGFGIHLIIS 205
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Uppothetical protein (carA 3' region) - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 29-Sep-1999 C;Accession: C55880  
R.Kwon, D.H.; Lu, C.D.; Walthall, D.A.; Brown, T.M.; Houghton, J.E.; Abdelal, A.T. A;Tile: Structure and regulation of the carAB operon in Pseudomonas aeruginosa and P A;Reference number: A5580; MUID: 94222830  
A;Reference number: A5580; MUID: 94222830  
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-216 cKWO> A;Residues: 1-216 cKWO> A;Cross references: GB:U04992; NID:q451649; PIDN:AAA19047.1; PID:g451652 C;Superfamily: hypothetical protein b1798
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C15pecies: Vibrio cholerae
C15pecies: Vibrio cholerae
C15pecies: Numbro cholerae
C15pecies: Numbro C15pecies: Vibrio cholerae
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62 LIIEKMAWLHTLIMVGGG---LYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKG 118
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C.Species: Bacillus halodurans
C.Species: Bacillus halodurans
C.Date: 01-Dec-2000
S.Accasion: B3703
R.Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
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A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A.Totacs: preliminary
A.Nolecule type: DNA
A.Toss-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04148.1; GSPDB:GNOG
G.Genetics: BH0429
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MEDLINE-97426617; PubMed-9278503;
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Science 277:1453-1474(1997).
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15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
14REDNINE EFFLUX PROTEIN.
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NU4M_BRAFL
PTPW_ECOLI
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CONCEPTUAL TRANSLATION.
Rudd K.E.;
Unpublished observations (DEC-1997).
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                 GenCore version
Copyright (c) 1993 - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 IEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKS---GRSFLKGLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 INLANPKAIIYFGSVFSLFVGDNVGTTARWGI----FALIIVETLAWFTVVASLFALPQMR 177
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SEQUENCE FROM N.A.
MEDILINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
"Whole-genome random sequencing and assembly of Haemophilus influenzae RG."; Science 269:496-512(1995).
-i. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-i. SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 210;
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P75693; P71307;
P75693; P71307;
O1-NOV-1997 (Rel. 35, Last sequence update)
U1-NOV-1998 (Rel. 35, Last sequence update)
HYPOTHETICAL 24.8 KDA PROTEIN IN BETT-PRPR INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
254D159014845473 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.0%; Score 368.5; DB 1
38.8%; Pred. No. 8.8e-23;
rative 42; Mismatches 73
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                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 47 AND 73.
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SEQUENCE FROM N.A.

STATAIN-RD / KW2C / AFCC 51907;

MEDLINE-95350630; PubMcd=7552800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Realayage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Otterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
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Bacteria; proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
NCBI_TaxID=727;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHERICAL PROTEIN HI3307.
                                                                                                                                                                                                                                                                                                              EMBL, M87049; AAA67619.1; ALT_FRAME.
EMBL, M30198; AAC76826.1; ALT_FRAME.
EMBL, M30198; ., NOT_ANNOTATED_CDS.
PIR, S30713; S30713;
ECGGENE; EG11468; rhtC.
InterPro; IPPR011123; ..
Framsport; Transport; Transpo
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150 1
206 AA;
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                          STRAIN—PAG1:

STRAIN—PAG1:

STRAIN—PAG1:

STORDINE—PAG137337:

PUBMED—10984043;

MIZOGUCHI S.D., Warrener P.,

Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

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Bricky M.J., Brinkman F.S.L., Tolger K.R., Kas A., Larbig K., Yuan Y.,

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Reizer J., Spherer D.H., Wong G.K.-S., Wu. Z., Paulzen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 LSLSNPKAILFFISFFIQFVDPGYAYPGLSFLVLAVILELVSALYLSFLIFTGVRLAAWF 185
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                                                                                                                                                                                                                                                                                             opportunistic pathogen.";
Nature 406:399-964(2000).
-i- SUBCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAS.
Escheriaichia coli.
Batteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
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P76249; 007971; 007969;
15-7UL-1998 (Rel. 36, Created)
15-7UL-1998 (Rel. 36, Last sequence update)
15-7UL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 23.2 KDA PROFEIN IN GAPA-RND INTERGENIC REGION.
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A - S (IN REF. 1).
K -> Q (IN REF. 1).
K -> Q (IN REF. 1).
W. A30A08E714591B8D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 TVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHL 202
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12 AA;
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Best Local Simi
Matches 64;
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YEAS_ECOLI
1D YEAS_B
AC P76249
DT 15-JUL
DT 15-JUL
DE HYPOTH
GN YEAS.
GN YEAS.
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                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Grage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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79 ITQCEEIFSLIRIVGGAYLLWFAWCSMR-----RQSTPQMSTLQQPISAPWYVFFRR 130
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Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Roberts D., Schraum S., Davis R.W.; Submitted (NOV-1996) to the EMBL/Geneank/NDBJ databases.
-1 - SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROFEIN (POTENTIAL).
-1 - SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-9422830; Pubmed-8169201;
Kwon D.-H., Lu C.-D., Walthall D.A., Brown T.M., Houghton J.E.
Abdelal A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivísion; Pseudomonadaceae;
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E17F5ABC31EE3F26 CRC64;
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llarity 28.2%; Pred. No. 3e-14;
Conservative 50; Mismatches 83;
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PERFLESE A

1D YER7_PERE STANDARD; PRT; 216 AA.

PERFLESE STANDARD; PRT; 216 AA.

DT 01-0CT-1994 (Rel. 30, Created)

DT 01-0CT-2000 (Rel. 40, Last sequence update)

DF 01-0CT-2000 (Rel. 40, Last sequence update)

DF 14757 (Rel. 40, Last sequence update)

OS PSEUGOMONDAS aeruginosa.

ON Bacteria; Proteobacteria; gamma subdivision; Pseudoconsas.

ON NCBL_TAXID=287;

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN MEDLINE-8422830; PubMed=8169201;

RN MEDLINE-8422830; PubMed=8169201;

RN MEDLINE-8422830; PubMed=8169201;

RN Abdelal A.T.;

Structure and regulation of the carAB operon in RT aeruginosa and Pseudomonas stutzeri: no untransland RN 12]
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85
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223 AA;
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X MEDLINE-97251358; PubMed-9097040;

X MEDLINE-97251358; PubMed-9097040;

X A Sazi H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,

X A Mizobuchi K., Mori H., Morimura K., Makade S., Nakamura Y.,

X Masbimnto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,

X Namanto Y., Horluchi T.,

X Takemoto K., Wada C.,

X Takemoto M., Sampei G.,

X Takemoto M., Sampei G.,

X Takemoto M., Morimoli T.,

X Takemoto M., Sampei G.,

X Takemoto M., Morimoli T.,

X Takemoto M., Sanguence of the Escherichia coli K-12 genome

Corresponding to the 40.1-50.0 min region on the linkage map.";

DNA Res. 3:379-392(1996).

X Takemoto M., Sundamanto M., Maka M.,

X Takemoto M., Sampei M.,

X Takemoto M., Sampei M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 IVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG-----VMVWAGIALLGLHLIIERM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 IFIVLVPGPNTLFVLKNSVSSGMKGGYLAACGVFIGDAVLMFLAWAGVATL----IKTT 72
                                              SEQUENCE FROM N.A.
SERALI AG1655;
STRAINE-9743667; PubMed-9278803;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Olunkett G. III, Bloch C.A., Rode C.K., Maybew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 212;
                                                                                                                                                        Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.0%; Score 190; DB 1; Length 21 28.2%; Pred. No. 1.4e-08; ive 36; Mismatches 85; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90823; BAA15593.1; -.
EMBL; D90824; BAA15602.1; -.
ECGGNE: EG13505; yeas.
InterPro; IPR001123; -.
Pfam; PF01810; LysE; 1.
Hypothetical protein; Transmem!
TRANSMEM 12 32 PP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mar.
Local Sir.
57;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VVIAKSVILFTIKYLGAAYLIYLG---VKSFFAKSMFSLDDMQSQAKNMASSPKRYYKT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 SFLKGLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII-VETLAWFTVVASLFA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 SFMGGSLSNILNPRTVLVYVTIMPOFINLNGNINQQLIILASILTLLAVLWFLFLVXIID 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LLAYIPIAAMMVII----PGADTMLVMKNTLRYGPKAGRYNILGLATGLSFWTVIAILGLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                       17.1%; Score 180.5; DB 1; Length 210; llarity 24.5%; Pred. No. 7.7e-08; Conservative 41; Mismatches 101; Indels 15;
                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 23.4 KDA PROTEIN IN AAPA-SIGV INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2A37D9419FDB0A58 CRC64;
                                                                                                                                                              Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
210 AA.
                                                                                                                                                                                          Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 299117; CAB14652.1; -.
EMBL; U93874; AAB80873.1; -.
Subtilist; BG12304; yrhP.
InterPro; IPR001123; -.
Pfan; PF01810; LySE; 1.
Hypothetical protein; Transmemi
TRANSMEM
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     STANDARD;
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210 AA;
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Matches 51; Conserv
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
YRHP_BACSU
005406;
                                                                                                                                                                                                                                                                                                               STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GLLTNLANPKAIIYFGSVFSLFVGDNVGT---TARWGIFALIIVETLAWFTVVASLFALP 174
                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20437337; PubMed-10984043;
Stover C. K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C. K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Rowalik D.J., Lagrou M., Garber R.L., Coltry L., Tolentino E., Westbrook-Wadman S., Yuan Y., Smith K.J., Spencer D.N., Folger K.R., Kas A., Larbig K., Lim R.W., Smith K.A., Spencer D.N., Folger K.E.W., Lory S., Olson M.V., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., Complete genome sequence of Pseudomonas aeruginosa PAOI, an Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PAO1;
Whitchurch C.B., Young M.D., Hobbs M., Mattick J.S.,
"Pseudomonas aeruginosa chemotactic transduction genes pill, chpA
chpB and downstream genes chpC, chpD and chpE.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPPORTURISALS FORMAGE OF THE STATE OF THE PROPERTY (POTENTIAL).

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROPEIN (POTENTIAL).

1. SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                   Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.1%; Score 159; DB 1; Length 203; 27.7%; Pred. No. 3.8e-06; Live 38; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
195553C048AAD099 CRC64;
                                                                   (Rel. 38, Last sequence update) (Rel. 40, Last annotation update) TRANSDUCTION PROTEIN CHPE.
                     203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                     PRT;
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66 PO
89 PO
143 PO
169 PO
21290 MW;
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EMBL, BAG0440; AAG03806.1; -.
InterPro; IPR001123; -.
Ffam: PF01810; LYSE; 1.
                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequ
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69
123
149
203 AA;
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                      Pseudomonas.
NCBI_TaxID=287;
                                                                                                                   CHPE OR PA0417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ransmembrane.
                                                                                                  CHEMOTACTIC
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                 PSEAE
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TRANSMEM
TRANSMEM
TRANSMEM
SEQUENCE
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Best Local 9
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CHPE_PSEAE
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                                                                                                                                                                                                                                                                                                                                         (1)
RA MYSTER STORE FROM N.A. Worden H., Tanaka A., Asamizu E., Nakamura Y.,
RA MYSTIAN N. Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
MYSTIAN N. Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
MYSTIAN N., Hirosawa M., Tabata M., Nakazaki N., Naruo K.,
RA Mystian N., Tabata S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.,
RA Yamada M., Yasuda M., Tabata S.,
RA Yamada M., Yasuda M., Tabata S.,
RA Yamada M., Tabata S.,
Ratrain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RT Synechocystis S., Strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RT Synechocystis A. S., Silog-136(1996).
II. SUBCELLULAR LOCATION: INTECRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE RHT FAMILY.
CC -1- SIMILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 LANPKAIIYEGSVESLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGY-- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 IIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 159; DB 1; Length 206; Similarity 26.6%; Pred. No. 3.9e-06; Conservative 39; Mismatches 96; Indels 56; Conservative 39; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF493754B8F264AF CRC64;
                                                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803).
Bacteria: Cyanobacteria; Chroococcales; Synechocystis.
NGBL_TAXID=1148;
                                                                                                                                         206 AA
                                                                                                                                                                            01-NOV-1997 (Rel. 35, created)
U-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat)
HYPOTHETICAL 22.0 KDA PROTEIN SLR1627.
175 QMRRG----YQRLAKWIDGFAGALFAGFGIHLI 203
                                     171 WLRRNTSLFWHRVS-----YAGCGVLLL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- ORLAKWIDGFAGALFAGFGIHLIIS
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 Pr
22041 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D90914; BAA18437.1; -.
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001123; -. Pfam; PF01810; LysE; 1. Hypothetical protein; TTRANSMEM 9 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 1
206 AA;
                                                                                                                                       YG27_SYNY3
P74343;
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Best Local Si
Matches 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 SIVFLAALFPQFIMPQQPQLMQYIVLGVT-----TIVVDIIVMIGXATLAQRIALWI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAWLHTLIMVGGGLYLCWMGYQMLRGALKKE-AVSAPAPQVELAKSGRSFLKGLLTNLAN 125
71 AFEVLKWAGAAYLIWLGIQQWRAAGAIDLKSLASTQSRRHL-----FQRAVFVNLTNPK 124
                                          AIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A. STRAIN=NCIME 1102; STRAIN=NCIME 1102; SWIĞIR S. KATLYSHEV A.V., Fish L., Durant E.L., Winson M.K., SWILLiams P., MacIntryre S., Stewart G.S.A.B.; Submitted (SEP-1966) to the EMBL/Genbank/DDBJ databases.
-i- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).-i- SIMILARTY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
17-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteobactería; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIC2C492CDA0179A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.6%; Score 111.5; DB
26.0%; Pred. No. 0.023;
iive 32; Mismatches
                                                                                                                                                                                                                                                                               206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
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                                                                                                                                 DG------FAGALFAGFGIHLIISR 206
                                                                                                                                                          EMBL; U65741; AAB70019.1; ALT_INIT.
InterPro; IPR001123; -.
InterPro; IPR001123; -.
FY00th FF10810; Lyse; Hypothetical protein; Transmembrane
                                                                                                                                                                                                                                                                               PRT;
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57
85
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108
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21505 MW;
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                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Aeromonas salmonicida
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116
148
185
206 AA;
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                                                                                                                                                                                                                                                                               YGGA_AERSA
P70775;
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Best Local Si
Matches 52,
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TGGA_AERSA
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                                                                                                                                                                                                                                                                                                   STRAIN=K12 / MG1655;
BEDLINE-2358231 PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
Analysis of the Escherichia coli genome: DNA sequence of the region
from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 MVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE RIF FAMILIA.
-i- CAUTION: THIS IS A CONCEPURAL TRANSLATION; A FRAMESHIFT HAD TO BE INTRODUCED IN POSITIONS 60 TO EXTEND THIS ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The novel transmembrane Escherichia coli proteins involved in the amino acid efflux.";
FEBS Lett. 452:228-233(1999).
-i- FUNCTION: CONDUCTS THE EFFLUX OF HOMOSERINE AND HOMOSERINE
                                                                                                                                                          Escherichia coli,
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
MEDILME-99313167; Pubmed-10386596;
Zakataeva N.P., Aleshin V.V., Tokmakova I.L., Troshin P.V.,
Livshits V.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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1164F17738509C8C CRC64;
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Similarity 20.7%; Pred. No. 5.5e-05;
13; Conservative 44; Mismatches 96;
                                                                                  15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HOMOSERINE/HOMOSERINE LACTONE EFFLUX PROTEIN.
                           206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M87049; AAA67620.1; ALT_FRAME.
EMBL; AE000458; AAC76827.1; ALT_FRAME.
PIR, S30714; S30714.
ECOGENE: EG11469; rhtB.
InterPro: IPR001123; -
Fram: PF01810; LysE; 1.
Transport; Transmembrane.
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                           PRT;
                                                                   (Rel. 23, Created)
(Rel. 38, Last sequ
(Rel. 38, Last anno
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                           STANDARD;
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/ MG1655;
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148
182
206 AA;
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TRANSMEM
RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 VDLLSNAAPIVLDIMRW-----GGIAYLLWFAVMAAKDAMTNK---VEAPQIIEETEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 TVPDDTPLGGSAVATDTRNRVRVEVSVDKORVWVKPMLMAIVLTWLNPNAYLDAFVFIGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194
                                                                                                                                      1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIA-LLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 ------ELAKSGRS-----AIIYFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 VFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 105; DB 1; Length 236:
ilarity 20.4%; Pred. No. 0.085;
Conservative 36; Mismatches 99; Indels
                                                                           Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL,
POTENTIAL,
POTENTIAL,
EE86E8CF037C4727 CRC64;
                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
LYSINE EXPORTER PROTEIN.
                 236 AA.
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                PRT;
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58
89
167
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25425 R
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=1718;
                               15-JUL-1998
15-JUL-1998
               LYSE_CORGL
P94633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 PKAIIYFGSVFSL-FVGDNVGTTARWGIFALIIVETLAWF-----TVVASLFALPQMRR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 MAWLHTLIMVGGGLYLCWMGYQMLRGALKKE-AVSAPAPQVELAKSGRSFLKGLLTNLAN 125
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=AI.
MEDLINE=97431471; PubMed=9286976;
MEDLINE=97431471; PubMed=9286976;
MEDLINE=97431471; PubMed=9286976;
Chhabra S.R., Williams P., Macintyre S., Stewart G.S.A.B.;
Chhabra S.R., Williams P., Macintyre S., Stewart G.S.A.B.;
Courum sensing in Aeromonas hydrophila and Aeromonas salmonicida:
identification of the LuxRI homologa AhyRI and Assarl and their
cognate N-acythomoserine lactone signal molecules.";
J. Bacteriol. 1979:5271-5281(1997).
J. Bacteriol. 1979:5271-5281(1997).
J. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
J. SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LAMIIPIGAQNAFVLSRGIHRNH-HLLTATLCCLCDLVLIGIGVFGGANLLAASPIGLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MXT-2000 (Rel. 39, Last annotation update)
40-MXT-2000 (Rel. 59, Last annotation update)
Acromonas hydrophila.
Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 225;
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POTENTIAL.
172DB104473B0B09 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 GYSKLLILLLVSPCWGWRCNWRAGLCWRHKAIFVPHLI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 104.5; DB
; Pred. No. 0.089;
29; Mismatches
  225 AA
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Interpro; PR001123; -...
Pfan: PF01810. LysE; J.
Hypothetical protein; Transmembrane.
  PRT;
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57 PO
85 PO
136 PO
170 PO
24482 MW;
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P11667;
01-0CT-1989 (Rel. 12, Created)
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116
150
225 AA;
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Best Local Similarity
Matches 57; Conserv
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YGGA_AERHY
P52047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 A----NPKAIIYFGSVFSLFVGDNVGTTARWGIFAL-IIVETLAWFTVVASLFA--LPQM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97426617; PubMed-9278503;
Blatiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
Alefounder P.R. Baldwin S.A., Perham S.A., Short N.J.;
Identification, molecular cloning and sequence analysis of a gene cluster encoding the class II fructose 1.6-bisphosphate aldolase, 3 phosphoglycerate kinase and a putative second glyceraldehyde 3-phosphoglycerate kinase of Escherichia coli.";
Mol. Microbiol. 37.73-732(1989).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
                                                              2
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 23.2 KDA PROTEIN IN SBM-FBA INTERGENIC REGION (ORF
                                                                                                                                             Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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25; Mismatches 93; Indels
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MEDLINE=89313302; PubMed=2546007;
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EMBL; AAC000375; AAC75960.1; -.
EMBL; X14436; CAA32607.1; -.
PIK; S04736; QQEC5A.
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InterPro; IPR001123; -.
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Pfam; PF01810; LysE; 1.
Hypothetical protein; TRANSMEM
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                                                                                                               Escherichia coli
                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                             Bacteria; Pi
Escherichia
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Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          James H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H., Kashimoto K., Kim S., Kimura S., Kiitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.; Tugami H., Bali K., Makamura W., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.; Submitted (Jan-1997) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97426617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rudd K.E.;
Unpublished observations (AUG-1994).
-! - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-! - SUBILARITY: BELONGS TO THE RHT FAMILY.
                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escheriohia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                  in
                                                                          01-OCT-1994 (Rel. 30, Created)
1-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 21.2 KDA PROTEIN IN SRMB-UNG INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                            "Non-ribosomal proteins affecting the assembly of ribosomes transfer in the second of ribosomes transfer in the second of ribosomes transfer in the second of ribosomes transfer in the second of ribosomes and respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nashimoto H., Saito N.; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   (In) Nierhaus K.H. (eds.);
the translational apparatus, pp.185-195, Plenum Press,
                                     195 AA.
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EMBL; D64044; -; NOT_ANNOTATED_CDS.
EMBL; AE000344; AAC75631.1; -.
EMBL; D90886; BAA16464.1; -.
ECGEDE: BG12445; yfix.
Hypothetical protein; Transmembrane.
TRANSMEM 8 28 POTENTIAL.
                                     PRT;
                                     STANDARD;
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                                                                                                                                                                           Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                               York (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION.
                                     YFIK_ECOLI
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RESULT 14
YFIK_ECOLI
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6, 2001, 14:41:21
                                      Query Match
Best Local Similarity
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Job time: 192 sec
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XX MEDLINE-#37RY;

XA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Cole S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F.,

RA Gordon S.V., Egglmeier K., Gas S., Hanry C.E. III, Tekaia F.,

B Hadcock K., Basham D., Erown D., Chillingworth T., Connor R.,

A DATISE R., Devilh K., Feltwall T., Gentles S., Hamin N., Holroyd S.,

RA Hornsby T., Jagaels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,

RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,

RA Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT "Decipher genome sequence";

RT Nature 393:537-544(1998.";

RA Nature 393:537-544(1998.";

CC "I SIMILARITY: BELONGS TO THE LYSEXYGGA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as 1 ony as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         62 ---FSLAVIDPAAVH-LLSWAGAAYIVWLAWKIATSPTKEDGLQA------KPISFW 108
                                                                                                                                                                                                                                             57 LLGLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFL 116
                                                                                                      Query Match 9.6%; Score 101; DB 1; Length 195;
Best Local Similarity 22.0%; Pred. No. 0.15;
Matches 39; Conservative 32; Mismatches 72; Indels 34; Gaps
                                                                                                                                                                          1 MLMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCG----VMVWAGIA 56
                                                                                                                                                                                                RV0488 OR MTCY2069.14.

Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                 117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL 173
                                                                                                                                                                                                                                                                                                                                         109 ASFALQEVNVKIILY------GVTA-LSTFVLPQTQALSWVVGVSVLLAM 151
  POTENTIAL.
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5F86B828DDDEC090 CRC64;
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E198975DF088E6E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0C7-1996 (Rel. 34, Created)
01-0C7-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 20.9 KDA PROTEIN RV0488.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 201 AA
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71 91 PO
142 162 PO
195 AA; 21248 MW;
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Y488_MYCTU
ID Y488_MYCTU
AC Q11154;
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                                                                                                                                                                                                                             63 IIEKMAWLHTLIMVGGGLYLCWMGYQML--RGALKKEAVSAPAPQVELAKSGRSFLKG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                101 OMCLVVTFLNPH--VYLLDTVVLIGALANEESDLRWFFGAGAWAASVVWFAVLG--FSAGR 156
                                                                                                                                                     92; Indels 33; Gaps
                                                                                                              3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHL 62
      Length 201;
ch 9.2%; Score 96.5; DB 1; Similarity 22.2%; Pred. No. 0.35; 47; Conservative 40; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 MRRGYQRLAKW -- IDGFAGALFAGFGIHLIIS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOPFFATPAAWRILDALVAVTMIGVAVVLVT 188
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SEQUENCE FROM N.A. STRAIN=SGSC1412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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99kr30 bacillus an
99kr75 bacillus an
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99kr40 vibrio chol
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99kr40 vibrio chol
99pgr vibrio chol
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99kr47 vibrio chol
99reff sagrobacteri
99kr47 vibrio chol
99reff vibrio chol
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Q9kvf5 vibrio chol
Q9k8s1 bacillus ha
Q9rif0 versinia en
Q916h7 brucella me
Q9kfp9 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                           US-09-466-935-4
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1 MLMLFLTVAMVHIVALMSPG......IDGFAGALFAGFGIHLIISR 206
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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                                                                              protein search, using sw model
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ralstonia s
pictothyris
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LIAEGGALFSAIKIGGGLYLVWYAYNWVRHRQELHMGMGAV---ATSSITPWYVF----- 116
  63 IIEKMAWLHTLIMVGGGLYLCWMGYQMLR-----GALKKEAVSAPAPQVELAKSGR 113
  IEKMAWLHTLIMVGGGLYLCWMGYQMLRGA--LKKEAVSAPAPQVELAKSGRS----FLK 117
  GLLINLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
   3 MLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHL 62
  4 LFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLI 63
  SFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFAL
   Yersinia enterocolitica (type 0:8).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
   Length 212;
  Indels
SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takani H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, APO01517; BAB06551.1; -.
SEQUENCE 210 AA; 23712 MW; C49C7DE7C86F6F75 CRC64;
   EMBL/GenBank/DDBJ databases
  0C18DA690C479702 CRC64;
   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
   25.6%; Score 269.5; DB 2; ilarity 28.1%; Pred. No. 5.3e-15; Conservative 52; Mismatches 80;
  27.7%; Score 292; DB 2; 32.4%; Pred. No. 7.3e-17;
  212 AA
   37; Mismatches
  POMRRGYORLAKWIDGFAGALFAGFGIHLI 203
   RGYQRLAKWIDGFAGALFAGFGIHLII 204
  PRT;
  22790 MW;
   Submitted (JAN-1995) to the
EMBL: Z47200; CAB61500.1;
INTERPO: PR001123; -.
PFAM; PFF01810; LySE; 1.
SEQUENCE 212 AA; 22790 1
  Bacteria; Proteobacteria;
Versinia.
  Query Match 27.7%
Best Local Similarity 32.4%
Matches 67; Conservative
  PRELIMINARY;
  Best Local Similarity
Matches 59; Conserv
  SEQUENCE FROM N.A. STRAIN-WA-314;
   NCBI_TaxID=34054;
  YFUD PROTEIN.
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Heidelberg J.R., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Ermolaeva M.D., Vamathevan J., Fass S., Qin H., Dragoi I., Sellers P.,
MCDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
  64 YLVKQQPMLFNLLQLAGGSYLLYLGAGALQSVWAQKNASTPTHSPAPSI-LGNRRQAFTK 122
  121 TNLSNPKAIIYFGSVFSLFVGDNVGAAARWGIFALITLETLAWFTVVASLFALPKMRRGY 180
   62 LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVS----APAPQVELAKSGRSFLK 117
  118 GLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMR 177
  Gaps
   2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
  Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
   "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
  ς.
..
   Length 222;
   Match 29.7%; Score 313.5; DB 2; Length Local Similarity 31.3%; Pred. No. 1.3e-18; les 62; Conservative 52; Mismatches 79; Indels
  222 AA; 23485 MW; B5B83AC3804E5E71 CRC64;
   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHERICAL PROTEIN VC0191.
   Last sequence update)
Last annotation update)
   Bacillus halodurans.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
  222 AA
   210 AA
  Created)
                                     PRT;
   99K851
99K851;
01-CCT-2000 (TrEMBLrel. 15, C
01-CCT-2000 (TrEMBLrel. 15, I
01-CCT-2000 (TrEMBLrel. 15, I
BH2932 PROTEIN.
  Nature 406:477-483(2000).
EMBL: AE004109; AAF93367.1;
IIGR: VC0191; -
  RGYORLAKWIDGFAGALF 195
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  PRELIMINARY;
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   PRT;
  46;
  182 RLAKWIDGFAGALFAGFGIHLI 203
   180 ARAVLIDRLSGLVLIALAIRVL 201
  Nature 406:477-483(2000).
EMBL; AEO04412; AAF96744.1; -.
TGR; VCA0846; -.
SEQUENCE 204 AA; 21719 MW;
  Conservative
   PRELIMINARY;
  PRELIMINARY;
  Similarity
   Vibrio cholerae.
  Best_Local Sim
Matches 51;
   cholerae.
  Query Match
   Q9KLAO;
  Q9RMX0
  Q9KLA0
  8
  RESULT
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   Eygmunt M.S., Diaz M.A., Teixeira-Gomes A.P., Cloeckaert A.; "Cloning, uncleotide sequence, and expression of the Brucella melitensis such gene coding for a dihydrolipoamide succinyltransferase homologous protein."; Submitted (FBB-2000) to the EMBL, GenBank/DDBJ databases. ERBL; AF235020; AAF43702.1; -. SEQUENCE 212 AA; 23158 MW; OC21287CEA665F56 CRC64;
  HTLIMVGGGLYLCWMGYQMLR-GALKKEAVSAPAPQVELAKSGRSFLK----GLLTNLAN 125
   126 PKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQRLAK 185
  Gaps
  Gaps
   11 VHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAWL 70
   14 IFVFAIVSPGADLAMVIRQSLLHGRREAIITSFGIGTALMMHVTYTVLGLGLIISRSIYL 73
   2 LMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
   01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2000 (TrEMBLrel. 15, Last annotation update)
AMINO ACID EFFLUX-LIKE PROTEIN.
Brucella melitensis.
Brucella recobacteria; alpha subdivision; Rhizobiaceae group;
NCBL_TaxID=29459;
  40;
  23.9%; Score 251.5; DB 2; Length 212;
ilarity 29.9%; Pred. No. 1.6c-13;
Conservative 41; Mismatches 88; Indels 9
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  SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001508; BAB04148.1;
   207 AA; 22317 MW; 9FED148C8E8DD3F0 CRC64;
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Last annotation update)
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Bacillus/Staphylococcus group; Bacillus.
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   01-OCT-2000 (TYEMBLrel. 15, 01-OCT-2000 (TYEMBLrel. 15, 01-OCT-2000 (TYEMBLrel. 15, BH0429 PROTEIN.
   | | | : | | : | | 190 WIDRTSGVVFIALGIKL 206
  186 WIDGFAGALFAGFGIHL 202
  PRELIMINARY;
  PRELIMINARY;
  BH0429.
Bacillus halodurans.
   Similarity
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   59;
  Query Match
Best Local S
Matches 63
   Query Match
   SEQUENCE
   Best Local
Matches 5
  09L6H7
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  Q9KFP9
  Q9L6H7
                        2
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  71
                 RESULT
10 0916H7
10 002 092
AC 099
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  SEQUENCE FROM N.A.
STRAIPEL TORN NIG961 / SEROTYPE 01;
STRAIPEL TORN NIG961 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Hafkey E.K., Peterson J.D., Umayam L.A.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Fraser C.M.;
   115
   119 LLTNLANPKALIYFGSVFSLFVGDNVGTTARWG------IFALIIVETLAWFT---- 165
  63 VVLHQSPVLFKTISYAGAAYLAYLGWNALR---SKGGVAAKLESGESVSVWQSAREGLLI 119
  62 LIIEKMAWLHTLIMVGGG---LYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKG 118
  62 LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT 121
   122 NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGYQ 181
   Gaps
  61
  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
   63 ALIYOSALAFTVVKYAGAAYLLYLAWKAFQE-----KGEGLSID-KQTTLA-YGALYKKG
  2 IMLFLIVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH
   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
   Length 204;
  Indels
   204 AA; 21719 MW; D09887299659FBBD CRC64;
  166 --WASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR 206
   175 QLLMRSSFIKNOMHR-----IKGGLLALIGLQVAFSK 206
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0846.
   18.7%; Score 197.5; DB 2; 25.2%; Pred. No. 4.4e-09;
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   205 AA.
  Mismatches
   204
   Q9RMX0;
01-MAY-2000 (TrEMBLrel. 13, Created)
   DA E
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LANDKAIIYFGSVFSLFVG-DNVGTTARWGIFALIIVETLAWFTVVASLFALPQMRRGY- 180
  16.6%; Score 174.5; DB 2; ilarity 29.1%; Pred. No. 4.2e-07; Conservative 37; Mismatches 80;
  181 ------QRLAKWIDGFAGALFAGFGIHLIISR 206
  SGTFRDRLLKNSRFNEYMNIAATIIFIGLGLKLMTTQ 207
   212 AA
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  PRT;
   PRT;
   radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002037; AAF11548.1;
   09KS40;
01-OCT-2000 (TrEMBLrel. 15,
   PRELIMINARY;
   PRELIMINARY;
  Deinococcus radiodurans.
   TIGR; DR1999; -.
INTERPRO; IPRO00719;
INTERPRO; IPR001123;
   Query Match
Best Local Similarity
Matches 65; Conserv
  SEQUENCE FROM N.A.
  NCBI_TaxID=1299;
  Q9KS40
   Q9RSX2
   RESULT 10
   RESULT 11
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  Q9KS40
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  63 IIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTN 122
  LIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT 121
  122 NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII--VETLAWFTVVASLFALPOMRRG 179
   119 DMLNPKATLFYLAIFTQVIEPNTNIFVQ-SVYGLTVWSVEIL-WHMVLVFFLTHKSVRNY 176
   3 MLFLITVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHL 62
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   2 IMLFLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLH 61
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OKinAR R.T., Cloud K., Hampton O., Hill K.K., Keim P., Lamke G.,
OKinAR R.T., Cloud K., Martinez Y., Svensson R., Tatum L.R.,
Brown A.E., Jackson P.J.
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF189935, AAF13668.1;
INTERPRO; IPR001123;
PPAM; PF01810; LysE; 1.
   30;
   17.6%; Score 186; DB 2; Length 208;
25.3%; Pred. No. 4e-08;
ive 49; Mismatches 83; Indels
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26.1%; Pred. No. 1.9e-08;
tive 50; Mismatches 92; Indels
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STRAIN=C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001519; BAB07214.1; --
SEQUENCE 208 AA; 23158 MW; CAD7A46D63B8E45A CRC64;
  205 AA; 22900 MW; 6DC91EE968B524B8 CRC64;
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09K775;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
DIHYDRODIPICOLINATE REDUCTASE.
  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
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Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1392;
   180 YORLAKWIDGFAGALFAGFGIHL 202
   177 FLSISHWIERVTGTALILLGIRL 199
   Query Match 17.69
Best Local Similarity 25.39
Matches 55; Conservative
   53; Conservative
  Bacillus halodurans.
   Bacillus anthracis.
  Best Local Similarity
   Plasmid.
SEQUENCE
   Query Match
  BH3495
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65 EKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVS-----APAPQVELAKSGRSFL 116
  117 KGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALI-------IVETLAW 163
   MEDLINE:
MEDLINE=20036896; PubWed=10567266;
White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Elsen D.A., Gainn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
  5 FLTVAMVHIVALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLII 64
  Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus
  Length 241;
   "Genome Sequence of the Radioresistant Bacterium Deinococcus radiodurans \mathrm{R1.}";
  PFAM; PF01810; LysE; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
SEQUENCE 241 AA; 25161 MW; A4017ABFEDB60374 CRC64;
   164 FTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR 206
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(TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
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AMINO ACID TRANSPORTER.
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  Xylella fastidiosa
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  01-0CT-2000
01-0CT-2000
01-0CT-2000
   Xylella
  09P9Z0
  RESULT 13
  Matches
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   3;
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STRAIN-EL TORN NIG601 / SEROTYPE 01;
STRAIN-EL TORN NIG601 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
Elmolaeva M.D., Vamathevan J., Pass S., Qin H., Bragol I., Sellers P.,
McDonald L., Utterback T., Flishmann R.D., Nierman W.C., White O.,
Fraser C.M.;
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STRAIN=EL TORN N16961 / SEROTYPE 01;
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.D., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonnald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
   74 IMVGGGLYLCWMGYQMLRGALKK----EAVSAPAPQVELAKSGRSFLKGLLTNLANPKAI 129
   130 IYFGSVFSLFVGDNVGTTARWGIFALI-IVETLAWFTVVASLFALPQMRRGYQRLAKWID 188
   132 VFYLAFLPQFINPDYSPLAQSLLMALIHFAIAMVWQCGLAGALSSAKNLLKNASFMRWME 191
  VALMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALLGLHLIIEKMAWLHTL 73
  Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
   "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.",
   'DNA sequence of both chromosomes of the cholera pathogen Vibrio
   Length 212;
   212 AA; 22832 MW; 1DBDCBA37566C394 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) HYPOTHETICAL PROTEIN VC1421.
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Last annotation update)
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tive 38; Mismatches 105
  209 AA.
  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last ann
HYPOTHETICAL PROTEIN VCA1000.
   PRT;
  Nature 406:477-483(2000).
EMBL; AE004221; AAF94578.1; -.
TIGR; VC1421; -.
  189 GFAGALFAGFGIHLIISR 206
  192 GTTGVVLVALGIKLLLEK 209
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   Nature 406:477-483(2000).
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les 47; Conserv
  Vibrio cholerae.
   NCBI_TaxID=666;
  Query Match
  SEQUENCE
   cholerae
   Q9KKV0
Q9KKV0;
   Best Loca
Matches
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RA MEDLINE-LUSO'LI; PUDMEG-1091047;

RA MEDLINE-LUSO'LI; PUDMEG-1091047;

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

Barros M.H., Bonaccorsi E.D., Boordin S., Bove J.M., Briones M.R.S.,

Burno M.R.P., Camargo L.E.A., Carraro D.M., Carrer H.,

Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Fraga J.S., Franca S.C., Franco M.C., Ferron J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Forbme M., Furlan L.R.,

RA Colauto M.W.P., Longueira M.L., Kemper E.L., Kitajima J.P.,

RA Krieger J.E., Kuramea E.E., Laigref F., Lambais M.R., Lette L.C.C.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,

Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

Nhani A.J., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

RA Goliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

RA Goliveira M.C., de Sa K.G., Santelli R.V., Savasaki H.E.,

RA Allada H., Van Silva A.M., da Silva F.R., Silva M.A., Truffi D., Tsai S.M., Tsuhako M.H.,

RA Allada H., Van Silva A.M., Werjovski Almeida S., Vettore A.L.,

RA Allada H., Van Silva A.M., Werjovski Almeida S., Vettore A.L.,

RA Mather 406:11157(200).

REBEL, AE004079; Are5515.1, - .

BURNIERPRO; IPRO01123; - .
  59 GLHLIIEKMAWLHTLIMVGGGLYLCWMGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKG 118
  61 GVSALIAMNPLALNVIHLLGGAYLLKMAWDCLRA----DAAQAPTLDEAQAVAKTFYQRA 116
   117 LVSNLLNPKALVFFVLFLPQFVSTNIAASSAEQMFALGMVLNVCGLLFNLLLVALIGVFG 176
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   3 MLFLTVAMVHIVA----LMSPGPDFFFVSQTAVSRSRKEAMMGVLGITCGVMVWAGIALL 58
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Last sequence update)
Last annotation update)
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  174 -----POMRRGYOR-----LAKWI 187
  177 RSLVDNQRFRTYQHKVMGAVFLLLALWM 204
   MEDLINE=20365717; PubMed=10910347;
   (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 15,
   54; Conservative
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STRAINEL TOR NIG961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E. K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Ralzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
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  63 AIILSSAVAFSAVKWLGAAYLVYLGVQSLLSMWRGGSTLKVSESVESDKN--VFVQGVIV 120
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   Laboratoire de Biologie Moleculaire des Plantes Superieures
University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Rhizobium.
  Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome GenomeBiology.com 1 (6), 0014.1-0014.7 (2000) contact: Virginie Viprey
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Fax: +44(0)1603450045
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Unpublished (1999)
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Library normalized by Jihwan Song
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: Kenopus clone distribution information for
this library can be found through Research Genetics, visit their
below when ordering this clone: Source lab clone id - xlnnga005b04
Seq primer: -40RP from Gibco
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
   Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
Hat Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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Location/Qualifiers
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BF614897.1 GI:11787968
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   ACCESSION
   REFERENCE
  AUTHORS
  VERSION
KEYWORDS
  FEATURES
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COMMENT

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(pases 1 to 443)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
   seq_documentation_block: 24-Jan-2001

LOCUS BG038404 443 bp mRNA EST 24-Jan-2001

DEFINITION d34408.yl Xenopus laevis gastrula non normalized Xenopus laevis DEFINITION d34A04 clone XENOPUS_SOURCE_ID:xlnnga009p16 5' similar to TR:Q9RSX2 Q9RSX2_CONSERVED HYPOTHETICAL PROTEIN. ;, mRNA sequence.
   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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203 CIATCTGCTCTACATGGGTGGAACACGCTGCAGGAGAATGGCGCGCTGA 252
   285 GCCCGCGTCATCGGTGAGGCGATCCTCATCAATCTGCTGAACCCGAAACT 334
  153 CIGCACACCAGGGGGTGGCCTTTAGCGTGGTCAAATATCTGGGGGTCGC 202
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  335 GTCGATCTTCTTTTGCCTTCCTGCCGCAGTTCATCGCGCCGGATGAGG 384
   103 TCGGCATCGTGCCGCATCTGCTCGCCGCCATCACCGGTCTTGCCGCCATC 152
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  47 ysGlyValMetValTrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIle 63
  64 IleGluLysMetAlaTrpLeuHisThrLeuIleMetValGlyGlyGlyLe 80
   80 uTyrLeuCysTrpMetGlyTyrGlnMetLeuArg......GlyAlaLeuL 95
1 others
  Percent Identity: 26.897
   u
  Length:
   Gaps:
96
   144 alGlyThrThrAlaArg.TrpGlyIlePheAla 154
  385 CINTGCCGACATGGCGCATGGTCGATCTCGGCC 417
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   from: 1
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  BG038404.1 GI:12480989
  Xenopodinae; Xenopus.
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m

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Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM4-SN0012-010
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  Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Madl, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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PM4-SN0012-010400-001-902 SN0012 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Romo.
1 (bases 1 to 535)
  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  282 AGATCGATGAAACGAGGCAGCCG......CAAAAAGCC 313
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Percent Similarity:
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   ACCESSION
VERSION
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   Email: estewatson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Cone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xinnga009p16
Seg primer: -40RP from Gioco
High quality sequence stop: 430.
Other_ESTs: dg34h08.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
  :::::: 111
182 CTGCACACCAGTGCGTTTTAGCGTGGTCAAATATCTGGGGGTCGC 231
  82 CCTTTCGCAGGGGGCGCGGGCGACGTCATTGCGGCTTTCGGCTGCACGC 131
  |||||||| :::||||:::::::: ||||:::
232 CTATCTGCTCTACATGGCGTGGAACACGCTGCAGGAGAATGGCGCGCGTGA 281
   132 resecarcescarerserescescareacestrices
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          COMMENT
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  FEATURES
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Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
14 a 176 c 133 g 92 t
   Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome ratios sequence was derived from the FAPESP/LICR Human Cancer Genome ratios sequence was derived from the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM4-SN0012-030 400-001-g02&t3=2000-04.03&t4=1)
Seq primer: puc 18 forward high quality sequence start: 8 High quality sequence stop: 533.
Location/Qualifiers
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(Dases 1 to 535)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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LOCUS AW863932 535 bp mRNA EST 22-MAY-2000
DEFINITION PM4-SN0012-030400-001-902 SN0012 Homo sapiens cDNA, mRNA sequence.
   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
   Shotgun sequencing of the human transcriptome with ORF expressed
  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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   Fax: +55-11-2707001
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  Brazil
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ACCESSION
VERSION
KEYWORDS
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COMMENT
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   JOURNAL
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enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
57 a 463 c 347 g 38 t
   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10151 row: h column: 19
High quality sequence stop: 182.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1305) NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
  BG116685 1305 bp mRNA EST 30-JAN-2001
602317876F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4417986
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AQ991044
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  selected (1-2
   This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Photorhabdus luminescens.
Photorhabdus luminescens
Bacteria; Protecobacteria; gamma subdivision; Enterobacteriaceae;
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   82 euCysTrpMetGlyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAla 98
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Contact: ffrench-Constant RH
Department of Baiology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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MEDLINE
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  FEATURES
   TITLE
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  VERSION
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  1 (bases 1 to 709)
Choudhary, M., Mackenzie, C., Nereng, K., Sodergren, E., Weinstock, G.M.
and Kaplan, S.
  orf
   736H1C0930305 Rhodobacter sphaeroides 2.4.1 genomic DNA library Rhodobacter sphaeroides genomic clone 736H1C0930305 similar to c (D64002), DNA sequence.
   Rhodobacter sphaeroides.
Rhodobacter sphaeroides
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   Low-resolution sequencing of Rhodobacter sphaeroldes 2.4.1T:
chromosome II is a true chromosome
Microbiology 143, 3085-3099 (1997)
   127 ......LysAlaIleIleTyrPheGlySerValPheSerLeuPheVal 140
  156
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ValSerAlaProAlaProGlnValGluLeuAlaLysSerGlyArgSerPh 115
   181
   170 euPheAlaLeuProGlnMetArgArgGlyTyrGlnArgLeuAlaLysTrp 186
   83 GGTTTTCCCCTGTGTTAAGTAAGCCGCTTTCTCAACGGATT..... 43
   Contact: Mackenzie, C.
Department of Microbiology and Molecular Genetics
The University of Texas Health Science Center
6431 Fannin St., Houston, TX 77006, USA
Tel: (713) 794-1742
Fax: (713) 794-1782
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   JOURNAL
   FEATURES
   TITLE
  COMMENT
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chromosome II of Rhodobacter sphaeroides (Choudhary et al., 1994. Journal of Bacteriology, 176:7694-7702). The cosmids were then digested with a variety of restriction enzymes (BamHI, EcoRI, BgILI, PSII, ECORY, NoI and DNASEI) and restriction fragments subcloned into the respective multiple cloning site sites of phluescript SK (-). Note BgILI fragments were subcloned into the pBluescript bamHI site. DNASEI fragments were subcloned into the EcoRV site. All subclones were transformed into E. coli XLIBlue MRF'. All fragments were then sequenced and the sequences where possible were assembled using the GCG program GELASSEMBLE.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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DEFINITION 601446314F1 NIH_MGC_65 Homo sapiens CDNA clone IMAGE:3850491 5
  Tissue Prourement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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  54 GlylleAlaLeuLeuGlyLeuHisLeuIleIleGluLysMetAlaTrpLe
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  4 LeuPheLeuThrValAlaMetValHisIleValAlaLeuMetSerProGl
   Length: 79
Gaps: 1
Percent Identity: 29.114
  664 TITCGACNICCTGCGTTATGGGGGGTGGTGCATATCTT 700
   70 uHisThrLeuIleMetValGlyGlyGlyLeuTyrLeu 82
  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
   to: 709
   Align seg 1/1 to: B07708 from: 1
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59.494
   Unpublished (1999)
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Ratio:
   Percent Similarity:
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TITLE
JOURNAL
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  FEATURES
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Average insert size 1.8 kb. Library constructed by Life
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  424 GGCGCTGGTACTGGCTGGGCTGGCTCAGGACCCCCGTTCACGTCCACAC 375
   90 euArgGlyAlaLeuLys...........LysGluAlaValSer 100
  .......ValGluLeuAlaLysSerGlyArgSerPheLeuLysGlyL 119
   119 euLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGlySerVal 135
   765 rerefecerrerereresesercererrecererreceserreces
  49
  73 LeuIleMetValGlyGlyGlyLeuTyrLeuCys.....TrpMe 85
  68 ......AlaTrpLeuHisThr 72
   85 t......GlyTyrGlnMetL 90
   13 IleValAlaLeuMetSerProGlyProAspPhePhePheValSerGlnTh 29
  42 ......ValLeuGlyIleThrCysGlyVal
   52 .TrpAlaGlyIleAlaLeuLeuGlyLeuHisLeuIleIleGluLySMet.
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Gaps: 13
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Location/Qualifiers
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  283 g
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   Technologies.
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US-09-466-935-4 x BE872275/rev
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Percent Similarity:
  Quality:
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  FEATURES
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Mathonal Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Lunpublished (1999)

Contact: Robert Strausbergenih.gov

Tissue Procurement: DCTD/Drp

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Ling Hong/Rubin Ling High quality sequence stop: 791.

High quality sequence stop: 791.
   /note-"Organ: lung; Vector: porB7; Site_1: XhoI; Site_2: BCOR; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/AhoI sites using the following 5' adaptor: GGCAGAGGAG; Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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  324 TTCTTCTTCAGCTTTGCCAAGATGGAGGACTCCCGCTCCGGGAATGGGGG
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/clone="InAGE:3946562"
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BE795531.1 GI:10216729
   174 AGCTGGCTGTCGCTG.....
   seq_name: gb_est78:BE795531
  136 PheSerLeuPheVal...
  mRNA sequence.
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  264
   EST
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œ

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117 ysGlyLeuLeuThrAsnLeuAlaAsnProLysAlaIleIleTyrPheGly 133
KEYWORDS
SOURCE
   FEATURES
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   163 TrpPheThrValValAla.....SerLeuPheAlaLeuProGlnMetAr 177
   411 CTGATGCTGAGGGGGATGACTTTGAACTTCTGGACCGAGTCGGAGCTGAG 460
  461 TCAGGCTGGACCCTAGGCAGTGCTAGGAGCCACTGAGGCCAGAGACTCCTT 510
  84 rpMetGlyTyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSer 100
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   861 ....GCTTCTACTTATTCGCTCTCTAGAGGCCCCCAAGGTCGGCAGCAGCT
  .. ThrAlaArgTrpGlyIlePheAlaLeuIleIleValGluThrLeuAla
   43 euGlyIleThrCysGlyValMetValTrpAlaGlyIleAlaLeuLeuGly
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   76 lGlyGlyGly......beuTyrLeuCysT
   .....TTAGGI
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VERSION
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Bukmanlala Eutheria Primates; Catarrhini; Hominidae; Homo.

Mammanlala Eutheria Primates; Catarrhini; Hominidae; Homo.

DRS III-Butheria Primates; Catarrhini; Hominidae; Homo.

MRIOMA Institutes of Health, Mammalian Gene Collection (MGC)

MALOMA Institutes of Health, Mammalian Gene Collection (MGC)

Toriaci: Robert Strausberg' Ph.D.

Toriaci: (301) 496-1550

Email: Robert Strausberg' Ph.D.

Tassee Procurement: APCC

CIONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llni.gov

Plate: LLCM1189 row: i column: 15

High quality sequence stop: 329.

Location/Qualifiers

1. 1149

Location/Qualifiers

1. 1149

Location/Qualifiers

1. 1140

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GGCACGAG(G). Size-selected >500bp for average insert size

1. RKb. Library constructed by Ling Hong in the laboratory

of Geral M. Rubin (University of California, Berkeley)

II RT (Life Technologies). Note: this is a NIH_MGC

Library.

THE FORM and STATE S
  908
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  764 TTTCTGTGGTAGTCGTGGGGGGACCCTATGG...TGTTGGAGTGGGCC 718
  ......TyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaValSe 100
  671
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   98
   717 TTTGTTGTATATTATAGTCGTGGTCTTCTCCGCGG...GCGGTTAC
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AUTHORS
TITLE
JOURNAL
COMMENT
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E. I. (bases 1 to 687)
Simmen, M. W., Leitgeb, S., Clark, V. H., Jones, S.J. and Bird, A.
Gene number in an invertebrate chordate, Ciona intestinalis
Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4437-4440 (1998)
E. 2 (bases 1 to 687)
Simmen, M.W., Leitgeb, S., Charlton, J., Jones, S.J., Harris, B.R.,
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  112 GlyArgSerPheLeuLysGlyLeuLeuThrAsnLeuAlaAsnProLysAl 128
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  162 AlaTrpPhe...ThrValValAlaSerLeuPheAlaLeu...........173
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SOURCE
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   3 (bases 1 to 687)
Simmen,M.W. and Bird,A.
Sequence analysis of transposable elements in the sea squirt, ciona
   Direct Submission
Submitted (28 FEB-1998) ICMB, University of Edinburgh, King's
Bulldings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
VCLARK@srv0.bio.ed.ac.uk
  4 (bases 1 to 687)
Clark,V.H., Leitgeb,S., Charlton,J., Tweedie,S., Simmen,M.W.
\operatorname{Clark}, V.H. and \operatorname{Bird}, A. Nonmethylated transposable elements and methylated genes in
  103 TIGGIICAGCGIGICIGAATCACTCTGGICAGIATICTIATCCCGCTCGC 152
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  Ratio:
  Percent Similarity:
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adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
292 c 259 g 215 t

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      07-AUG-2000

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      07-AUG-2000

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      VERSION
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  161
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Average insert size 1.6 kb. Constructed by Life
Average insert size 1.6 kb. Constructed by Life
195 c 201 g 178 t
NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenh.gov.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov c column: 15
High quality sequence stop: 653.
I. 720

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// Anganism="Mus musculus"
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  74
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  87 .....TyrGlnMetLeuArgGlyAlaLeuLysLysGluAlaVal.....
  100 ... SerAlaProAlaProGln... ValGluLeuAlaLysSerGlyArgSe
  425 C.....ACAAATCTTCATCTTCCAGGAACCAAGGG
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  557 GCAG......CTGAGGTGGTCAGGCAAAAGACAAGAAA
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JOURNAL
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Mammalia; Euberia; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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   153 PheAlaLeullelleValGluThrLeuAlaTrpPheThrValValAlaSe 169
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401 .....CAAGGATTAGACCCCACGTGAGGTCAGGGGTTGGAGATGAAACT 357
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  111::: 11111 | 1112 | 1113 | 114 | 114 | 114 | 114 | 115 | 114 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 115 | 1
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1.099
43.085
  seq_name: gb_est89:BF584020
  356 ATAGTAGAGAGG 345
  203 IlelleSerArg 206
  house mouse.
   Quality:
Ratio:
   Percent Similarity:
  alignment_scores
   EST.
   VERSION
KEYWORDS
SOURCE
ORGANISM
   REFERENCE
  100
  130
  169
  126
```

us-09-466-935-4.rst